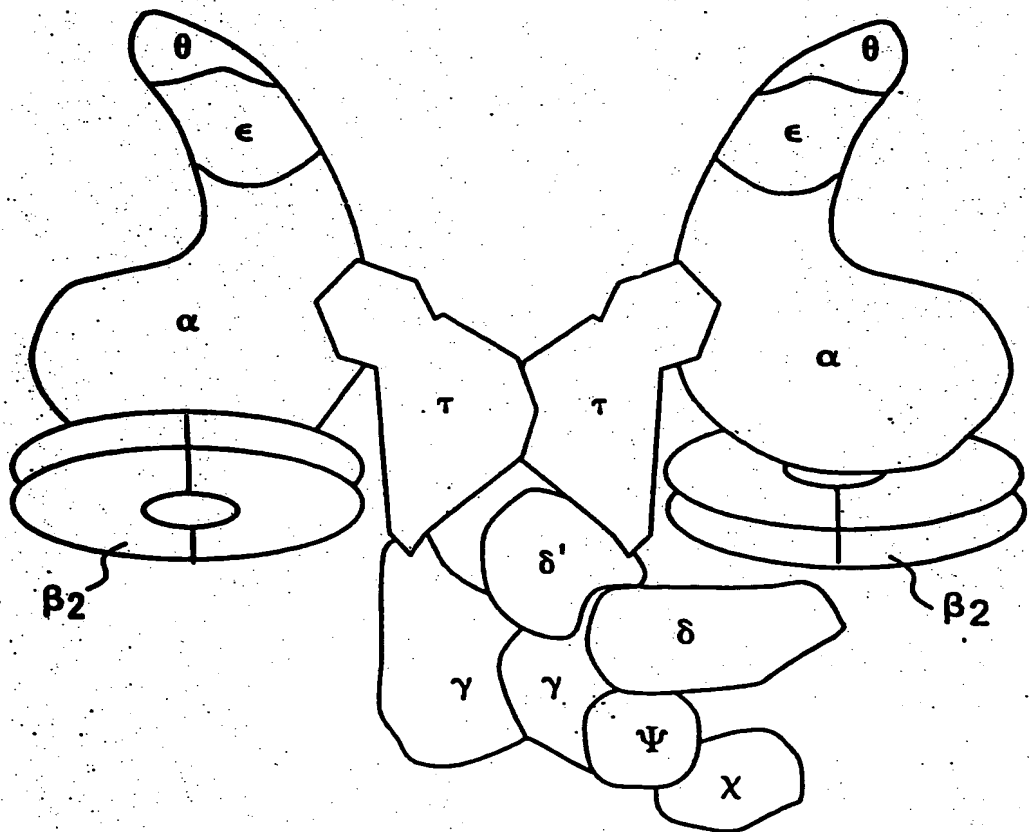


FIG.1



ATP binding

E. coli
 MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRHHAYLFSGTRGVGKTSIARLLAK
 B. subtilis
 MSYQALYRVFRPQRFEDVVGQEHITKTLQNALLOKKFSHAYLFSGPRGTGKTSAAKIFAK
 *** *

E. coli
 GLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRF
 B. subtilis
 AVNCEHAPVDEPCNECAACKGITNGSISDVIEIDAASNNGVDEIRDVKVAFPSAVTY
 *** *

E. coli
 KVYLIDEVHMLSRHSFNALLKTLLEPPPEHVKFLATTDPQKLPVTILSRCLQFHLKALDV
 B. subtilis
 KVIIDEVHMLSIGAFNALLKTLLEPPPEHCIFILATTEPHKIPLTIISRCQRFDFKRITS
 *** *

FIG. 2

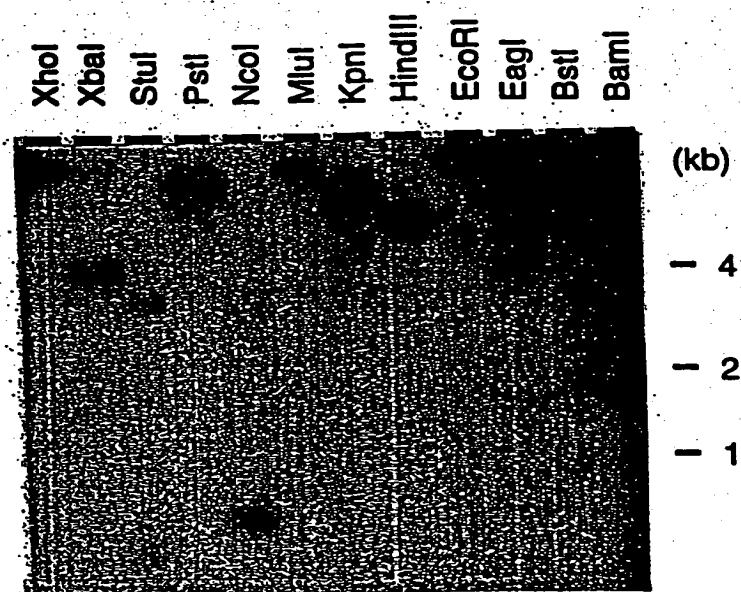


FIG.3

TCCGGGGGTG	GGGTCCCCAG	GTAGACCCCG	GCCCCTCQCG	TGAGCCCCTT	TACCCAGGCC	60
GCCACCTCCT	CCAGGGGGGC	CAAGCGGTGC	AAGGAGAGGA	ACGTCCGCAC	<u>CAGCCCCTAT</u>	120
					S.D.	
ACTAGCCTT	GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG					180
	met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val					(17)
					CAC	
GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG						240
gly gln glu his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln						(37)
GCS TAC CTS TTC TCC GGS AC						
GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC						300
ala tyr leu phe ser gly pro arg gly val gly lys thr thr ala arg leu leu ala						(57)
ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG						360
met ala val gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala						(77)
GtG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCG AGC AAC AAC TCC GTG						420
val gln arg gly ala his pro asp val val asp ile asp ala ala ser asn ser val						(97)
GAG GAC GTG CCG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG						480
glu asp val arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys						(117)
					C	
GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG						540
val phe ile leu asp Glu ala his met leu ser lys ser ala phe asn ala leu leu lys						(137)

FIG.4A-1

TGS CTS CTC CTC GGS GGS CTC GTG	CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG	600
ACC CTG GAG GAG CCC CCG CCC CAC GTG	CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG	(157)
thr leu glu glu pro pro his	val phe ala thr thr glu pro glu arg	
ATG CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CTC ACG GAG GAG		660
met pro pro thr ile leu ser arg thr gln his phe arg phe arg leu thr glu glu		(177)
GAG ATC GCC TTT AAG CTC CCG CGC ATC CTC GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG		720
glu ile ala phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu		(197)
GCC CTC CTC CTC GCG CTC GCG GCG GAC GCG GCG GCG GCG GAA AGC CTC CTG		780
ala leu leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu		(217)
GAG CGC TTC CTC CTC GAA GGC CCC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC		840
glu arg phe leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly		(237)
TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCG TCC CTC GCG AGG GGG AAA ACG GCG		900
ser pro pro gly thr gly val ala glu ile ala ser leu ala arg gly lys thr ala		(257)
GAG GCC CTC GGC CTC GCG CCG CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTC GTG		960
glu ala leu gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val		(277)
TCG GGC CTT TTG GAG GTG TTC CCG GAA GGC CTC TAC GCC GCG TTC GGC CTC GCG GGA ACC		1020
ser gly leu leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr		(297)
CCC CTT CCC GCC CCG CCC CAG GCC CTCG ATC GCC GCG ATG ACC GCC CTCG GAG GCC ATG		1080
pro leu pro ala pro pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met		(317)

FIG. 4A-2

GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA	1140
glu arg leu ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly	(337)
AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC	1200
arg ala leu ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly	(357)
CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG	1260
pro lys pro glu ser pro pro thr pro pro glu pro arg pro glu ala pro asp leu	(377)
CGG GAG CCG TGG CGG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CGG	1320
arg glu arg trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg	(397)
GAG GCC CGC CCG GAG GTC CCG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC	1380
glu ala arg pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala	(417)
TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT	1440
phe his tyr arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his	(437)
frameshift site	
TTC GGG GTG GAG GAG GTC GTC CTC GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG	1500
phe gly val glu glu val leu val leu glu gly glu lys lys ser leu ser pro arg	(457)

FIG.4B-1

CCC CGC CGG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA	1560
pro arg pro ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu val	(477)
GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CCG GTG GTC CGC CTC	1620
glu ala glu glu ala ala glu ala pro glu glu ala leu arg arg val arg leu	(497)
CTG GGG GGG CCG GTG CTC TGG GTG CCG CCG AGG ACC CCG GAG GCG CCG GAG GAG GAA	1680
leu gly gly arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu	(517)
CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA	1740
pro leu ser gln asp glu ile gly gly thr gly ile *	(529)
CGACCTCGGA CAAGAGACCG TGGACAACAT CCTCAAGCGC CTCCGCCGTA TTGAGGGCCA	1820
GGTGCGGGG CTCCAGAAGA TGGTGGCCGA GGGCCGCCCC TGCACGAGG TCCTCACCCA	1880
GATGACCGCC ACCAAGAAG CCATGGAGGC GCGGCCACC CTGATCCTCC ACGAGTTCCT	1940
GAACGTCTGC GCCGCCGAGG TCTCCGAGGG CAAGGTGAAC CCCAAGAAGC CCGAGGAGAT	2000
CGCCACCATG CTGAAGAACT TCATCTA	2027

FIG.4B-2

GGG	CAG	GAG	CAC	GTG	AGC	GCC	CTC	TAC	CGC	CGC	TTC	CGC	CCC	CTC	ACC	TTC	CAG	GAG	GTG	GTG	51
GCC	TAC	CTC	TTC	TCC	GTG	AAG	GAG	CCC	CTC	CTC	AAG	GCC	ATC	CGG	GAG	GGG	AGG	CTC	GCC	CAG	111
ATG	GCG	GTG	GGG	TGC	TGC	CAG	GGG	GAA	GAC	CCC	CCT	TGC	GGG	GTG	ACC	GGG	CAC	TGC	CAG	GCC	171
GtG	CAG	AGG	GGC	GCC	TGC	CAC	CCG	GAC	GTG	GTG	GAC	ATT	GAC	GCC	GCC	AGC	AAC	TCC	GTG	231	
GAG	GAC	GTG	CGG	GAG	CTG	GAG	CTG	GAA	AGG	ATC	CAC	CTC	GCC	CCC	CTC	TCT	GCC	CCC	AGG	AAG	291
GTC	TTC	ATC	CTG	GAC	CTG	GAC	GCC	CAC	ATG	CTC	TCC	AAA	AGC	GCC	TTC	AAC	GCC	CTC	CTC	AAG	351
ACC	CTG	GAG	GAG	CCC	CCC	CCC	CTC	CAC	GTG	CTC	TTC	GTG	TTC	GCC	ACC	ACC	GAG	CCC	GAG	AGG	411
ATG	CCC	CCC	ACC	ATC	ATC	CTC	TCC	CGC	ACC	CGC	CAC	TTC	CGC	TTC	CGC	CGC	CTC	ACG	GAG	GAG	471
GAG	ATC	GCC	TTT	AAG	CTC	CTC	CGG	CGC	ATC	CTG	GAG	GCC	GTG	GGG	CGG	GAG	GCG	GAG	GAG	GAG	531
GCC	CTC	CTC	CTC	CTC	CTC	CTC	CGC	CTG	GCG	GAC	GGG	GCC	CTT	AGG	GAC	GCG	GAA	AGC	CTC	CTG	591
GAG	GCG	TTC	CTC	CTC	CTC	CTG	GAA	GGC	CCC	CTC	ACC	CGG	AAG	GAG	GTG	GAG	CGC	GCC	CTA	GGC	651
TCC	CCC	CCA	GGG	ACC	GGG	ACC	GGG	GTG	GCC	ATC	GCC	GCC	TCC	CTC	GCG	AGG	GGG	AAA	ACG	GCG	711
GAG	GCC	CTG	GGC	CTC	CTC	GCC	CGG	CGC	CTC	TAC	GGG	GAA	GGG	TAC	GCC	CCG	AGG	AGC	CTG	GTC	771
TCG	GGC	CTT	TTG	GAG	GAG	GTG	TTC	CGG	GAA	GGC	CTC	GCC	TAC	GCC	TTC	GGC	CTC	GCG	GGA	ACC	831
CCC	CTT	CCC	GCC	CCG	CCG	CCC	CAG	GCC	CTG	ATC	GCC	GCC	ATG	ACC	GCC	CTG	GAC	GAG	GCC	ATG	891
GAG	GCG	CTC	GCC	CGC	CGC	CGC	TCC	GAC	GCC	TTA	AGC	CTG	GAG	GTG	GCC	CTC	CTG	GAG	GCG	GGA	951
AGG	GCC	CTG	GCC	GCC	GCC	GAG	GCC	CTA	CCC	CAG	CCC	ACG	GGC	GCT	CCT	TCC	CCA	GAG	GTC	GGC	1011
CCC	AAG	CCG	GAA	AGC	AGC	CCC	CCG	ACC	CCG	GAA	CCC	CCA	AGG	CCC	GAG	GAG	GCG	CCC	GAC	CTG	1071
CGG	GAG	CGG	TGG	CGG	CGG	GCC	TTC	CTC	GAG	GCC	CTC	TGC	AGG	CCC	ACC	CTA	CGG	GCC	TTC	CGG	1131
GAG	GCC	CGC	CGC	GAG	GTC	CGG	CGG	GAA	GGC	CAG	CTC	GTG	AGG	CTC	CTC	CCC	GAG	GAC	AAG	GCC	1191
TTC	CAC	TAC	CGC	AAG	GCC	GTC	TCG	GAA	CAG	AAG	GTG	AGG	CTC	CTC	CCC	CTG	GCC	CAG	GCC	CAT	1251
TTC	GGG	GTG	GAG	GAG	GTC	GTG	CTC	CTC	GTG	CTG	GAG	GGA	GAA	AAA	AGC	CTG	AGC	CCA	AGG	AGG	1311
CCC	GCG	CCG	GCC	CCA	CCT	CCT	CCT	GAA	GCG	CCC	GCA	CCC	CCG	GGC	CCT	CCC	GAG	GAG	GTA	GTA	1371
GAG	GCG	GAG	GAA	GCG	GAG	GAG	GAG	GAG	GAG	GCC	CCG	GAG	GAG	GCC	TTG	AGG	CGG	GTG	CGC	CTC	1431
CTG	GGG	GGG	GGG	GGG	GGG	GGG	CTC	TGG	GTG	CGG	CGG	CCC	AGG	ACC	CGG	GAG	GCG	CCG	GAG	GAA	1491
																					1551

CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA (1590)

FIG.4C

Met	ser	ala	leu	tyr	arg	arg	phe	arg	pro	leu	thr	phe	gln	glu	val	gly	gln	glu	20	
his	val	lys	glu	pro	leu	leu	lys	ala	ile	arg	glu	gly	arg	leu	ala	gln	ala	tyr	leu	40
phe	ser	gly	pro	arg	gly	val	gly	lys	thr	thr	thr	ala	arg	leu	leu	ala	met	ala	val	60
gly	cys	gln	gly	glu	asp	pro	pro	cys	gly	val	cys	pro	his	cys	gln	ala	val	gln	arg	80
gly	ala	his	pro	asp	val	val	asp	ile	asp	ala	ala	ser	asn	asn	ser	val	glu	asp	val	100
arg	glu	leu	arg	glu	arg	ile	his	leu	ala	pro	leu	ser	ala	pro	arg	lys	val	phe	ile	120
leu	asp	glu	ala	his	met	leu	ser	lys	ser	ala	phe	asn	ala	leu	leu	lys	thr	leu	glu	140
glu	pro	pro	pro	his	val	leu	phe	val	phe	ala	thr	thr	glu	pro	glu	arg	met	pro	pro	160
thr	ile	leu	ser	arg	thr	gln	his	phe	arg	phe	arg	arg	leu	thr	glu	glu	glu	ile	ala	180
phe	lys	leu	arg	arg	ile	leu	glu	ala	val	gly	arg	glu	ala	glu	glu	glu	ala	leu	leu	200
leu	leu	ala	arg	leu	ala	asp	gly	ala	leu	arg	asp	ala	glu	ser	leu	leu	glu	arg	phe	220
leu	leu	leu	glu	gly	pro	leu	thr	arg	lys	glu	val	glu	arg	ala	leu	gly	ser	pro	pro	240
gly	thr	gly	val	ala	glu	ile	ala	ala	ser	leu	ala	arg	gly	lys	thr	ala	glu	ala	leu	260
gly	leu	ala	arg	arg	leu	tyr	gly	glu	gly	tyr	ala	pro	arg	ser	leu	val	ser	gly	leu	280
leu	glu	val	phe	arg	glu	gly	leu	tyr	ala	ala	phe	gly	leu	ala	gly	thr	pro	leu	pro	300
ala	pro	pro	gln	ala	leu	ile	ala	ala	met	thr	ala	leu	asp	glu	ala	met	glu	arg	leu	320
ala	arg	arg	ser	asp	ala	leu	ser	leu	glu	val	ala	leu	leu	glu	ala	gly	arg	ala	leu	340
ala	ala	glu	ala	leu	pro	gln	pro	thr	gly	ala	pro	ser	pro	glu	val	gly	pro	lys	pro	360
glu	ser	pro	pro	thr	pro	pro	pro	pro	arg	pro	glu	glu	ala	pro	asp	leu	arg	glu	arg	380
trp	arg	ala	phe	leu	glu	ala	leu	ala	leu	arg	thr	leu	arg	phe	val	arg	glu	ala	arg	400
pro	glu	val	arg	glu	gly	gln	lys	val	arg	leu	phe	pro	glu	asp	lys	ala	phe	his	tyr	420
arg	lys	ala	ser	glu	gln	lys	val	arg	leu	leu	pro	leu	ala	gln	ala	his	phe	gly	val	440
glu	glu	val	val	leu	val	leu	glu	gly	glu	lys	lys	ser	leu	ser	pro	arg	pro	arg	pro	460
ala	pro	pro	pro	glu	ala	pro	pro	ala	pro	gly	pro	pro	glu	glu	glu	val	glu	ala	glu	480
glu	ala	ala	glu	glu	ala	pro	glu	glu	ala	leu	arg	arg	val	val	arg	leu	leu	gly	gly	500
arg	val	leu	trp	val	arg	arg	pro	arg	thr	arg	glu	ala	pro	glu	glu	glu	pro	leu	ser	520
gln	asp	glu	ile	gly	thr	gly	thr	gly	ile											529

FIG.4D

Met	ser	ala	leu	tyr	arg	arg	pro	leu	thr	phe	gln	gln	val	gly	gln	glu	20
his	val	lys	glu	pro	leu	lys	ala	ile	arg	glu	gly	arg	leu	ala	tyr	leu	40
phe	ser	gly	pro	arg	gly	val	lys	thr	thr	ala	arg	leu	ala	met	ala	val	60
gly	cys	gln	gly	glu	asp	pro	cys	gly	val	cys	pro	his	cys	gln	ala	val	80
gly	ala	his	pro	asp	val	asp	ile	asp	ala	ala	ser	asn	asn	ser	val	glu	100
arg	glu	leu	arg	glu	arg	ile	leu	ala	pro	leu	ser	ala	pro	arg	lys	val	120
leu	asp	glu	ala	his	met	leu	ser	lys	ser	phe	asn	ala	leu	leu	lys	thr	140
glu	pro	pro	pro	his	val	leu	phe	val	ala	thr	thr	glu	pro	glu	arg	met	160
thr	ile	leu	ser	arg	thr	gln	his	phe	arg	phe	arg	leu	thr	glu	glu	ile	180
phe	lys	leu	arg	arg	ile	leu	glu	ala	val	gly	arg	glu	ala	glu	glu	ala	200
leu	leu	ala	arg	leu	ala	asp	gly	ala	leu	arg	ala	glu	ser	leu	leu	arg	220
leu	leu	leu	glu	gly	pro	leu	thr	arg	lys	glu	val	glu	arg	ala	leu	ser	240
gly	thr	gly	val	ala	glu	ile	ala	ala	ser	leu	ala	arg	gly	lys	thr	ala	260
gly	leu	ala	arg	arg	leu	tyr	gly	gly	glu	tyr	ala	pro	arg	ser	leu	val	280
leu	glu	val	phe	arg	glu	glu	gly	leu	tyr	ala	phe	gly	leu	ala	gly	thr	300
ala	pro	pro	gln	ala	leu	ile	ala	ala	met	thr	ala	leu	asp	glu	ala	met	320
ala	arg	arg	ser	asp	ala	leu	ser	leu	glu	val	ala	leu	leu	glu	ala	gly	340
ala	ala	glu	ala	leu	pro	gln	pro	thr	gly	ala	pro	ser	pro	glu	val	gly	360
glu	ser	pro	pro	thr	pro	glu	pro	pro	arg	pro	glu	ala	pro	asp	leu	arg	380
trp	arg	ala	phe	leu	glu	ala	leu	ala	arg	pro	thr	leu	arg	ala	arg	glu	400
pro	glu	val	arg	glu	gly	gln	leu	leu	cys	leu	phe	pro	glu	asp	lys	ala	420
arg	lys	ala	ser	glu	gln	lys	val	arg	leu	pro	leu	ala	gln	ala	his	phe	440
glu	glu	val	val	leu	val	leu	glu	glu	lys	lys	pro	asp	pro	lys	ala	pro	460
gly	pro	thr	ser														464

FIG.4E

Met	ser	ala	leu	tyr	arg	arg	pro	leu	thr	phe	gln	glu	val	val	gly	gln	glu	20			
his	val	lys	glu	pro	leu	lys	ala	ile	arg	glu	gly	arg	leu	ala	gln	ala	tyr	leu	40		
phe	ser	gly	pro	arg	gly	val	lys	thr	thr	thr	ala	arg	leu	ala	met	ala	val	60			
gly	cys	gln	gly	glu	asp	pro	cys	gly	val	cys	pro	his	cys	gln	ala	val	gln	arg	80		
gly	ala	his	pro	asp	val	asp	ile	asp	ala	ala	ser	asn	asn	ser	val	glu	asp	val	100		
arg	glu	leu	arg	glu	arg	ile	leu	ala	pro	leu	ser	ala	pro	arg	lys	val	phe	ile	120		
leu	asp	glu	ala	his	met	leu	ser	lys	ser	ala	phe	asn	ala	leu	lys	thr	leu	glu	140		
glu	pro	pro	pro	his	val	leu	phe	val	phe	ala	thr	thr	glu	pro	glu	arg	met	pro	pro	160	
thr	ile	leu	ser	arg	thr	gln	his	phe	arg	phe	arg	arg	leu	thr	glu	glu	ile	ala	180		
phe	lys	leu	arg	arg	ile	leu	glu	ala	val	gly	arg	glu	ala	glu	glu	ala	leu	leu	200		
leu	leu	ala	arg	leu	ala	asp	gly	ala	leu	arg	asp	ala	glu	ser	leu	leu	arg	phe	220		
leu	leu	leu	glu	gly	pro	leu	thr	arg	lys	glu	val	glu	arg	ala	leu	gly	ser	pro	pro	240	
gly	thr	gly	val	ala	glu	ile	ala	ala	ser	leu	ala	arg	gly	lys	thr	ala	glu	ala	leu	260	
gly	leu	ala	arg	arg	leu	tyr	gly	glu	gly	tyr	ala	pro	arg	ser	leu	val	ser	gly	leu	280	
leu	glu	val	phe	arg	glu	gly	leu	tyr	ala	ala	phe	gly	leu	ala	gly	thr	pro	leu	pro	300	
ala	pro	pro	gln	ala	ala	ile	ala	ala	met	thr	ala	leu	asp	glu	ala	met	glu	arg	leu	320	
ala	arg	arg	ser	asp	ala	leu	ser	leu	glu	val	ala	leu	leu	glu	ala	gly	arg	ala	leu	340	
ala	ala	glu	ala	leu	pro	pro	thr	gly	ala	pro	ala	pro	ser	pro	glu	val	gly	pro	lys	pro	360
glu	ser	pro	pro	thr	pro	glu	pro	pro	arg	pro	glu	ala	pro	asp	leu	arg	glu	arg	380		
trp	arg	ala	phe	leu	glu	ala	leu	arg	pro	thr	leu	arg	ala	phe	val	arg	glu	ala	arg	400	
pro	glu	val	arg	glu	gly	gln	leu	cys	leu	ala	phe	pro	glu	asp	lys	ala	phe	his	tyr	420	
arg	lys	ala	ser	glu	gln	lys	val	arg	leu	pro	leu	ala	gln	ala	his	phe	gly	val	440		
glu	glu	val	val	leu	val	leu	glu	gly	lys	lys	lys	ala							454		

FIG.4F

		ATP site	
E.coli	MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRHHAYLFSGTRGVGKTSIARLLAK		60
H.inf.K.....II.....KDN.L.....F..		60
B.sub.A.Y.VF...R.E.....ITKT.Q.A.LOKKFS.....P.T....A.KIF..		60
C.cres.	DA.T.....Y..R..E.LI...AMVRT...AF.T...A..FMLT.V.....TT.....R		113
M.gen.	-MH..FYQ.Y..IN.KQTL...SIRKI.V.AINRDKLPNG.I...E..T...TF.KII...		59
T.th.	--VSA.Y.RF..L..QE.....KEP.LKAIRE..LAQ.....P.....TT.....M		58

	Zn ⁺⁺ finger		
	* * *		
E.coli	GLNCET----	GITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPA	116
H.inf.VH-----	V.....E.E..KA....N.I.....E.....K.V	116
B.sub.	AV...H----	APVDE..NE.AA.KG.TN.SIS.V.....NNG.DEI..IR.K.KF..S	116
C.cres.	A..Y..DTVK.PSVDLTTEGYH..S.IE..HM.VL.L.....DEM.E...G.R...V		173
M.gen.	AI..LN----	WDQIDV.NS..V.KS.NTNSAI.IV.....KNGIN.I.E.VE..FNH.F	115
T.th.	AVG.QG-----	EDP.....PH.QAVQR.AHP.VVD.....NNS...V.E.RERIHL..L	112

E.coli	RGRFKVYLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATDPQKLPVTILSRCLQFHLK	176
H.inf.	V.....Y.....	176
B.sub.	AVTY...I.....IGA.....CI.I...E.H.I.L.I...QR.DF..	176
C.cres.	EA.Y...I.....TAA.....P.A..IF...EIR.V.....QR.D.R	233
M.gen.	TFKK...IL..A...TTQ.WGG.....S.PY.L.IFT..EFN.I.L.....QS.FF..	175
T.th.	SAPR..FIL..A....KSA.....P..L.VF...E.ERM.P.....TQH.RFR	172

FIG.5A

E.coli	ALDVEQIRHQLEHILNEEHIAHEPRALQLLARAAEGSLRDALSLTDQAIASGDGQ--VST	234
H.inf.	...ET...SQH.A...TQ.N.PF.DP.VK..K.Q..I..S.....M..R.--.TN	234
B.sub.	RITSQA.VGRMNK.VDA.QLOV.EGS.EII.S..H.GM.....L.....SFSGDI--LKV	234
C.cres.	RVEPDVLVKHFDR.SAK.GARI.MD..A.I.....V..G...L.....VQTERGQT.TS	293
M.gen.	KITSDL.LER.ND.AKK.K.KI.KD..IKI.DLSQ.....G...L..LAI.LIVKKL.LL	235
T.th.	R.TE.E.AFK.RR..EAVGREA.EE..L...L.D.A...E..LERFLLLEGP---LTR	229
E.coli	QAVSAMLGTLDDDDQALSIVEAMVEANGERMALINEAAARGIEWEALLVEMGLLHRIAM	294
H.inf.	NV..N...L...NYSVDILY.LHQG...LL.RTLQRV.DAAGD.DK..G.CAEK...Q..L	294
B.sub.	EDALLIT.AVSQLYIGK.AKSLHDK.VSDALETL..LLQQ.KDPAK.IED.IFYFRDMLL	294
C.cres.	TV.RD...LA.RS.TIA.Y.HVMAGKTKDALEGFRALWGF.ADPVVMLDV.DHC.AS.V	353
M.gen.	MLKKHLISLIEMQN.L.L.KQFYQ.I	260
T.th.	KE.ERA..SPPGTGVAEIAASLARGKTAELG.ARRLYGE.YAPRS.VSGL.EVFRGLY	289

FIG.5B

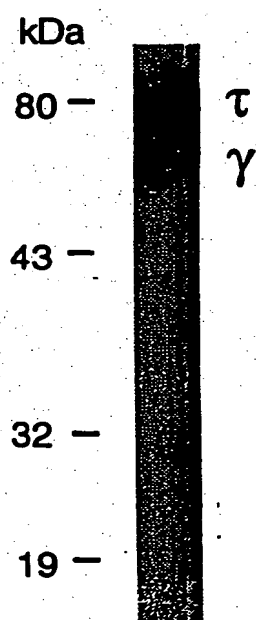
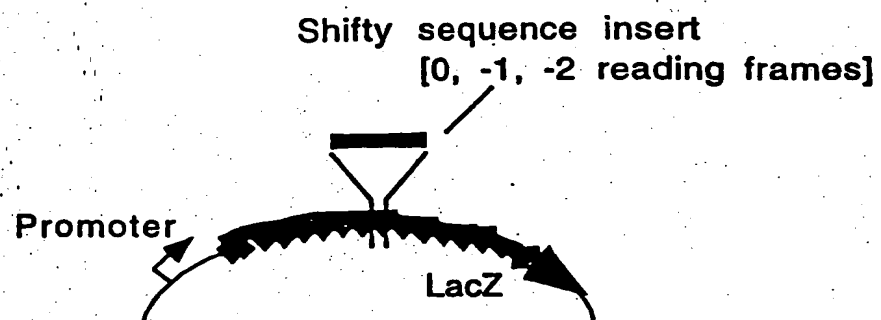


FIG.7

FIG.8A



	Reading frame	Blue	White
Shifty sequence	0	+	
	- 1	+	
	- 2	+	
Mutant sequence	0	++	
	- 1		+
	- 2		+

FIG.8B

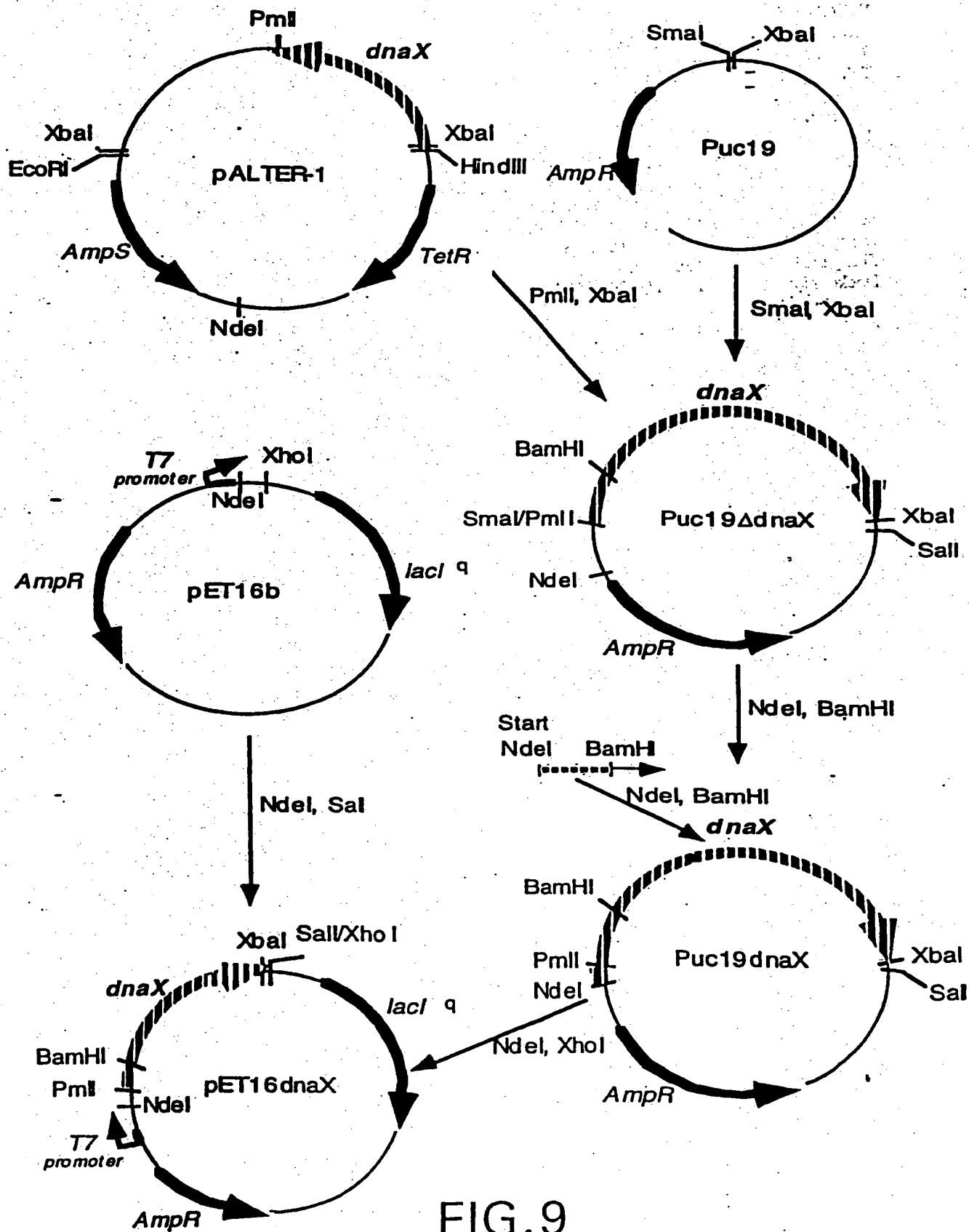


FIG.9

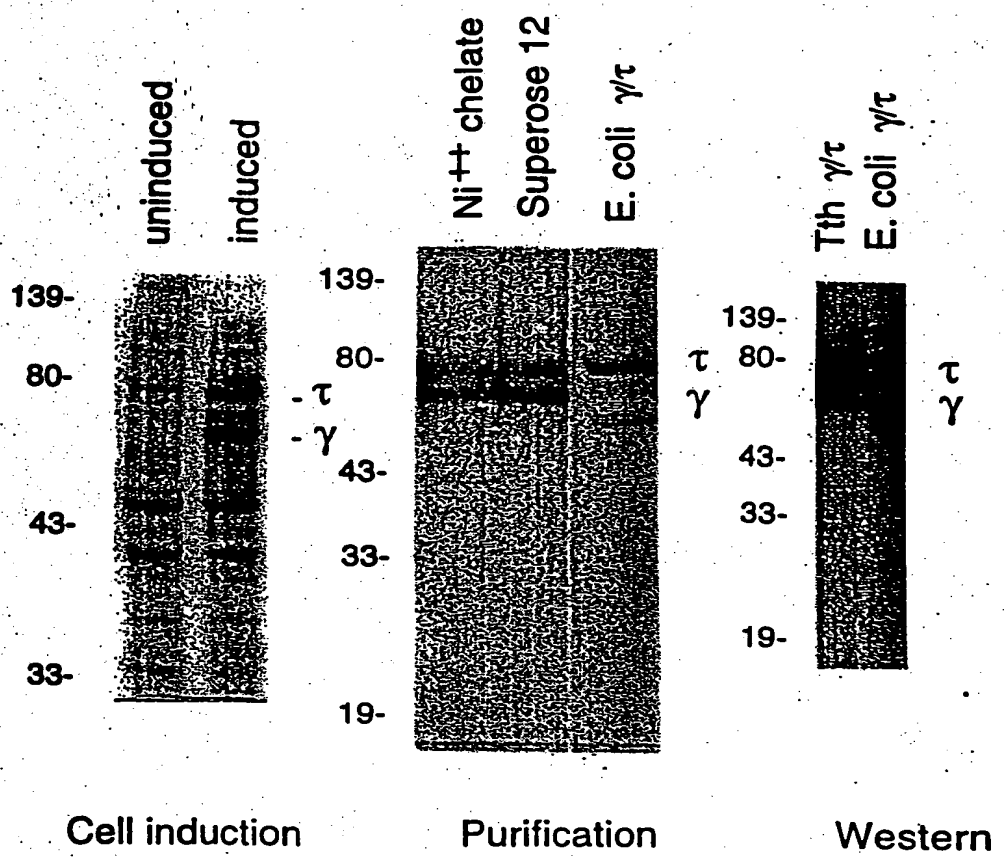


FIG.10A FIG.10B FIG.10C

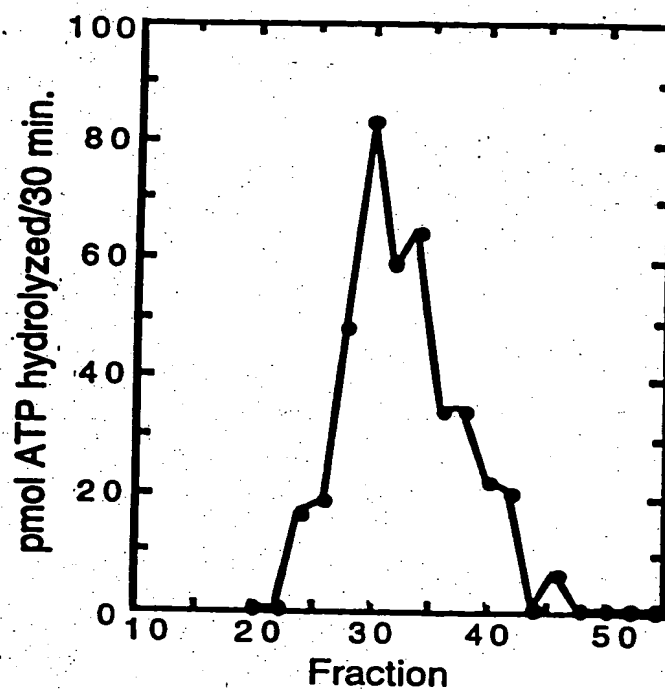


FIG. 11A

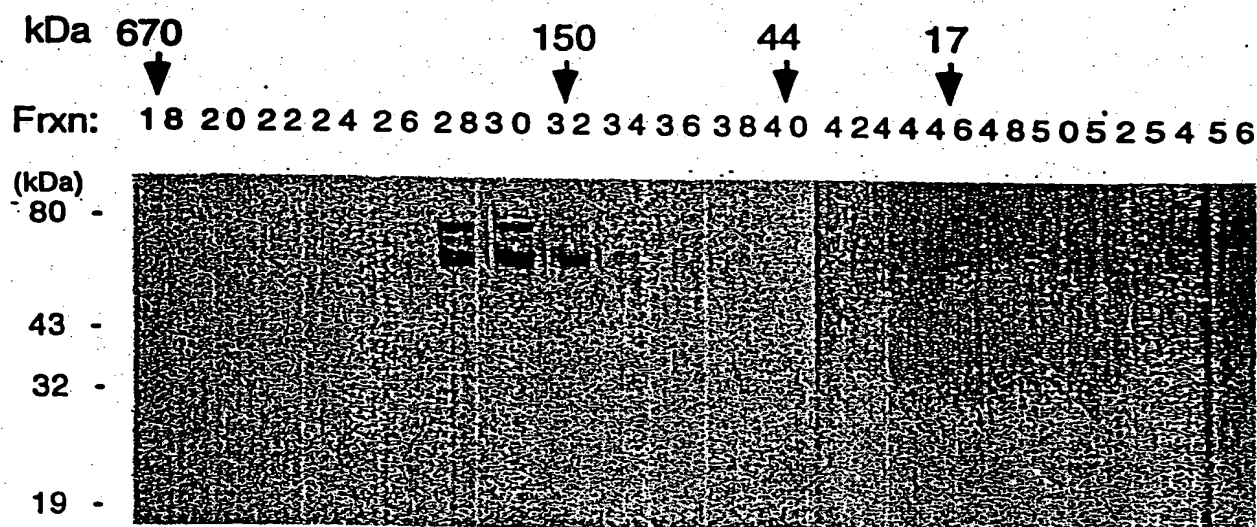


FIG. 11B

FIG.12A

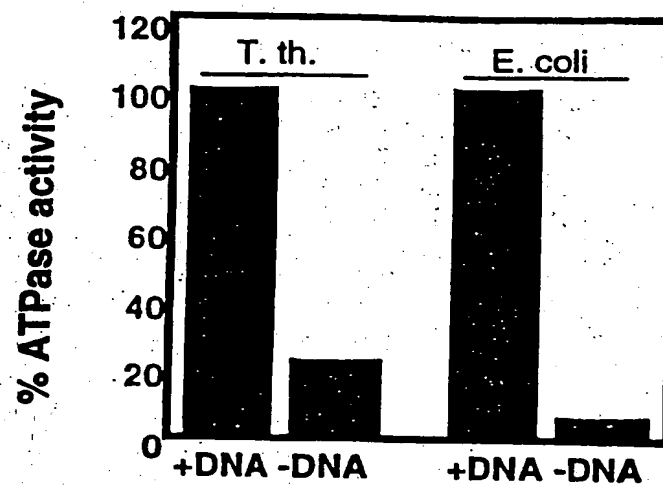


FIG.12B

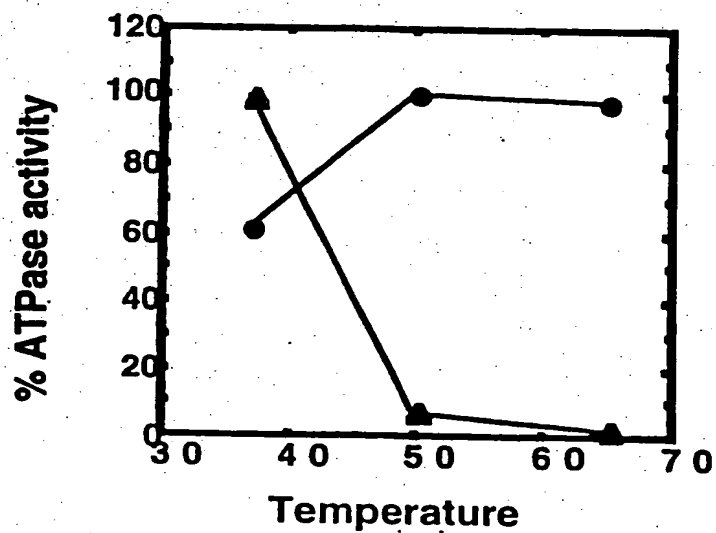


FIG.12C

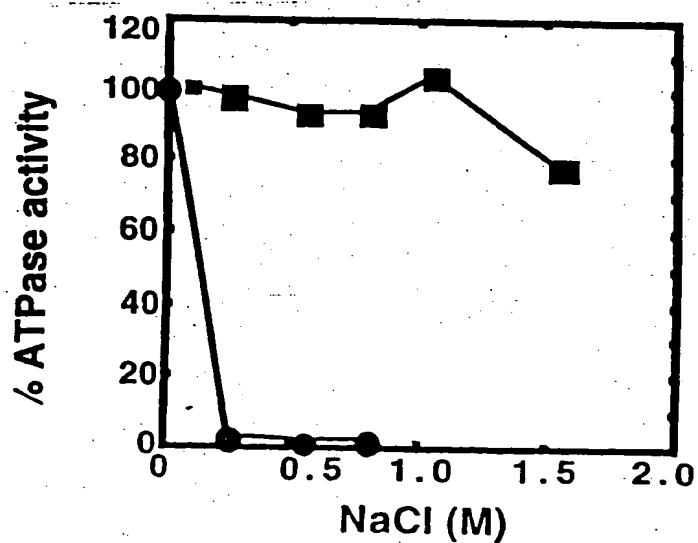


FIG.13A

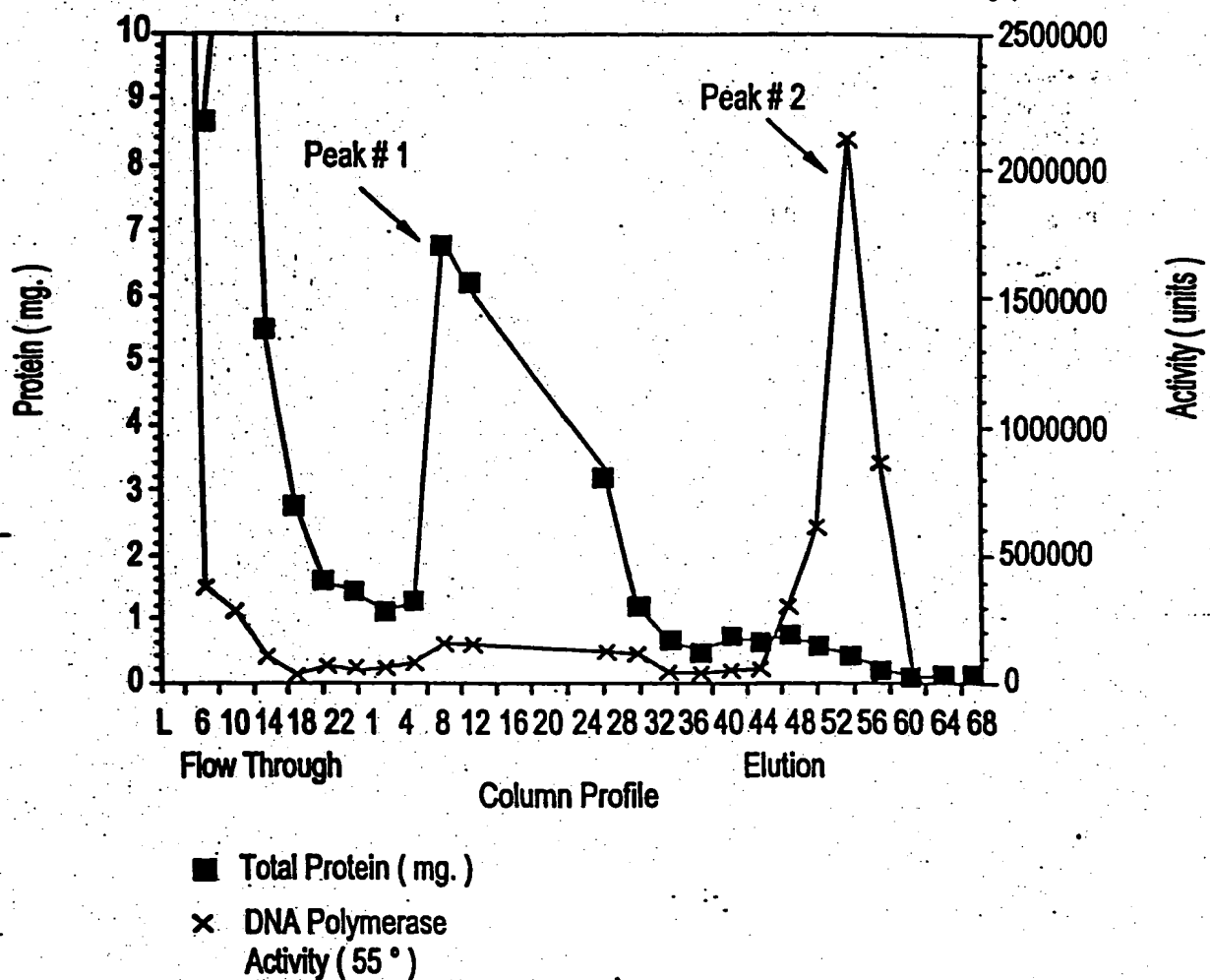


FIG.13B

ATP Agarose Step Column

FIG.13C

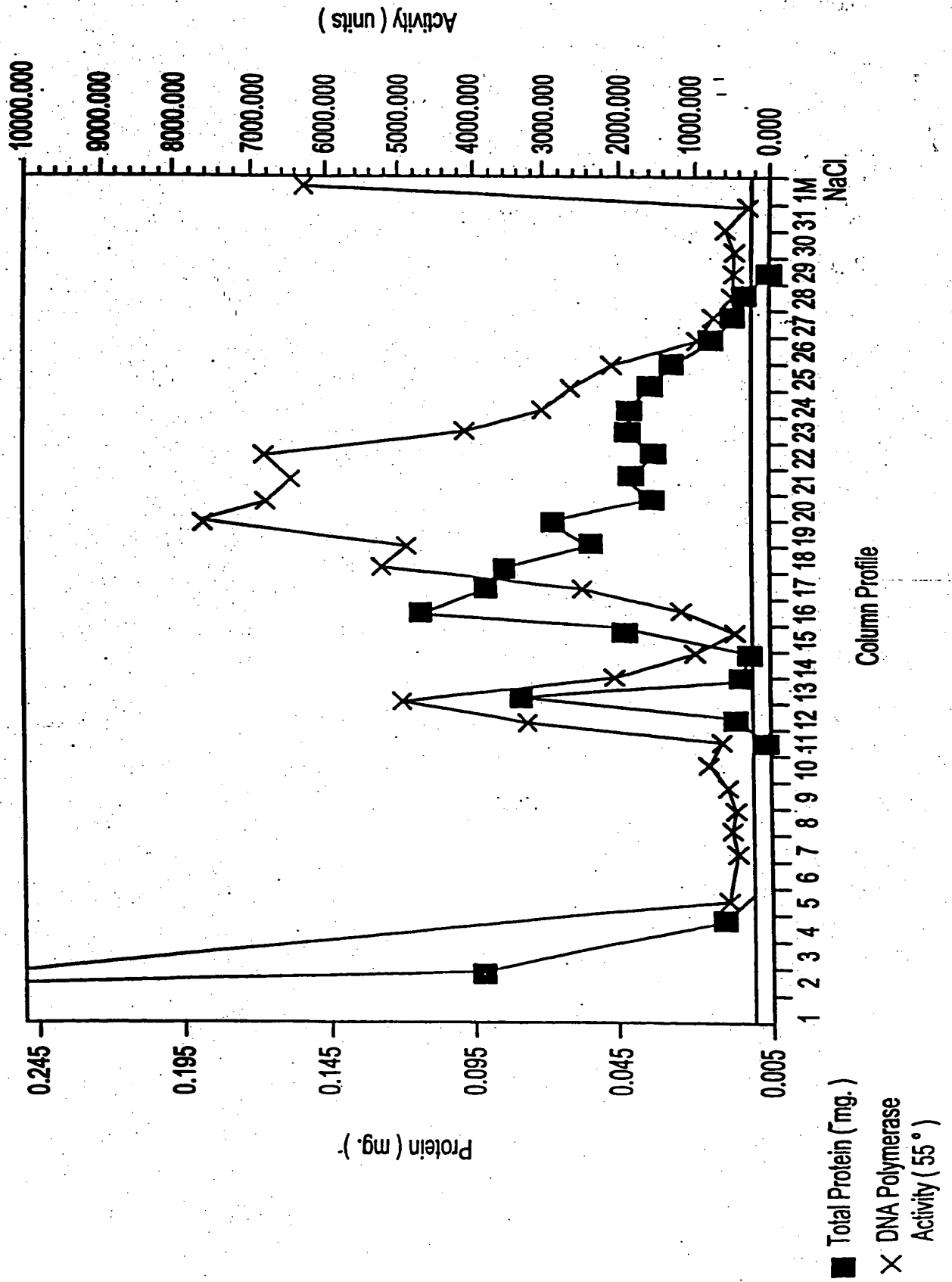
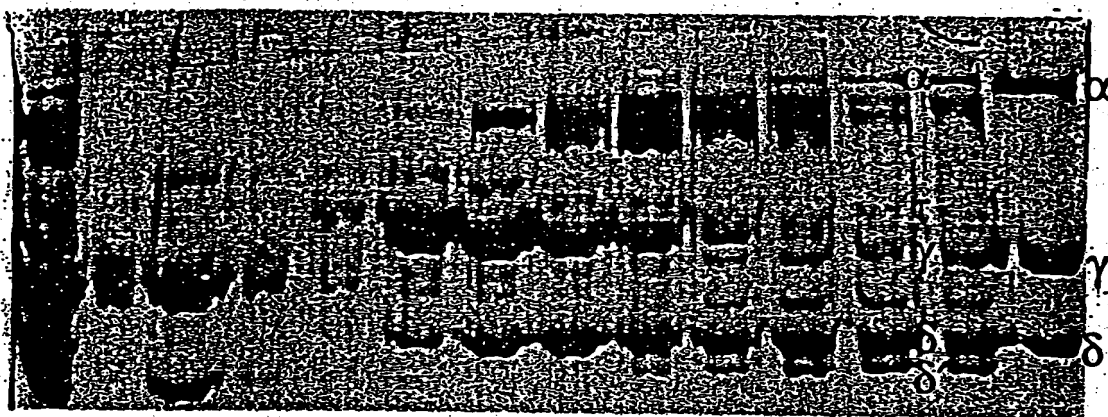


FIG.14A

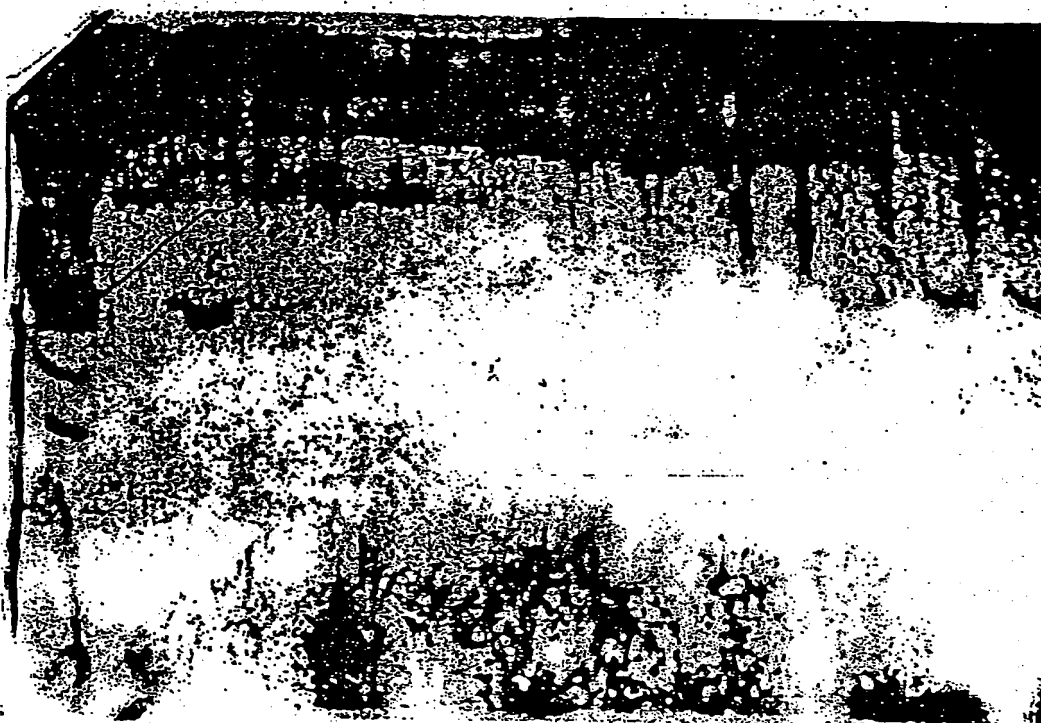
load FT 9 10 11 12 13 14 15 16 17 18 19 E. coli
α γ δ



↑ ↑
T.th E. coli
subunits subunits

FIG.14B

load FT 9 10 11 12 13 14 15 16 17 18 19



← α

Alignment of TTH1 with alphas subunits of other organisms.

E.coli	DRYFLELIRTGRPDEESYLHAAVELAEARGLPV	197	(ID#72)
V.chol.	DHFYLELIRTGRADEESYLHFALDVAEQYDLPV	197	(ID#73)
H.inf.	DHFYALSRTPNEERYTQAALKLAERCDPLV	197	(ID#74)
R.prow.	DRFYFEIMRHDLPPEEQFIENSYIQIASELSIPIV	195	(ID#75)
H.pyl.	DDFYLEIMRHGILDQRFIDEQVIKMSLETGLKII	213	(ID#76)
S.sp.	DDYYLEIQDHGSVEDRLVNINLVKIAQELDIKIV	202	(ID#77)
M.tub.	DNYFLELMDHGLTIERRVRDGLLEIGRALNIPPL	220	(ID#78)
T.th.	FFIEIQNHGLSEQK		(ID#61)

FIG.15A

Alignment of TTH2 with alphas subunits of other organisms.

E.coli	NKRRAKNGEPPLDIAAIPLDKKSFDMLQRSETTAVFQLESRGMKD	618	(ID#79)
V.chol.	NPRLKKAGKPPVRIEAIPLDDARSFRNLQDAKTTAVFQLESRGMK	618	(ID#80)
H.inf.	NVRMVRGKPRVDIAAIPLDPPESFELLKRSETTAVFQLESRGMKD	618	(ID#81)
R.prow.	CKKLLKEQGIKIDFDDMTFDDKTTYQMLCKGKGVGFQFESIGMKD	624	(ID#82)
H.pyl.	LKIITQHKISVDFLSLDMDDPKVYKTIQSGDTVGIFQIES-GMFQ	648	(ID#83)
S.sp.	QERKALQIRARTGSKKLPDDVKTKHLLLEAGDLEGIFQLESQGMKQ	643	(ID#84)
M.tub.	IDNVNRNGIDLDESVPDLDKATYELLGRGDTLGVFQLDGGPMRD	646	(ID#85)
T.th.	RVELDYDALTLDD		(ID#60)

FIG.15B

ATGGGCCGGGAGCTCCGCTTCGCCCACCTCCACCAGCACA	
CCCAGTTCTCCCTCCTGGACGGGGCGGCGAAGCTTTCGA	120
CCTCCTCAAGTGGGTCAAGGAGACGACCCCGAGGACCCC	
GCCTTGGCCATGACCGACCACGGCAACCTCTTCGGGGCCG	240
TGGAGTTCTACAAGAAGGCCACCGAAATGGGCATCAAGCC	
CATCCTGGGCTACGAGGCCTACGTGGCGGCGGAAAGCCGC	360
TTTGACCGCAAGCGGGGAAAGGGCCTAGACGGGGGCTACT	
TTACACTCACCCTCCTCGCCAAGGACTTCACGGGGTACCA	480
GAACCTGGTGCGCCTGGCGAGCCGGGCTTACCTGGAGGGG	
TTTTACGAAAAGCCCCGGATTGACCGGGAGATCCTGCGCG	600
AGCACGCCGAGGGCCTCATCGCCCTCTCGGGGTGCCTCGG	
GGCGGAGATCCCCCAGTTCATCCTCCAGGACCGTCTGGAC	720
CTGGCCGAGGCCCCGGCTCAACGAGTACCTCTCCATCTTCA	
AGGACCGCTTCTTCATCGAGATCCAGAACCACGGCCTCCC	840
CGAGCAGAAAAAGGTCAACGAGGTCTCAAGGAGTTCGCC	
CGAAAGTACGGCCTGGGGATGGTGGCCACCAACGACGGCC	960
ATTACGTGAGGAAGGAGGACGCCCGCGCCACGAGGTCTT	
CCTCGCCATCCAGTCCAAGAGCACCTGGACGACCCCGGG	1080
CGCTGGCGCTTCCCCTGCGACGAGTTCTACGTGAAGACCC	
CCGAGGAGATGCGGGCCATGTTCCCCGAGGAGGAGTGGGG	1200
GGACGAGCCCTTTGACAACACCGTGGAGATCGCCCGCATG	
TGCAACGTGGAGCTGCCCATCGGGGACAAGATGGTCTACC	1320
GAATCCCCCGCTTCCCCCTCCCCGAGGGGCGGACCGAGGC	
CCAGTACCTCATGGAGCTCACCTTCAAGGGGCTCCTCCGC	1440
CGCTACCCGGACCGGATCACCGAGGGCTTCTACCGGGAGG	
TCTTCCGCCTTTTGGGGAAGCTTCCCCCCCACGGGGACGG	1560
GGAGGCCTTGGCCGAGGCCTTGGCCCAGGTGGAGCGGGAG	
GCTTGGGAGAGGCTCATGAAGAGCCTCCCCCTTTGGCCG	1680
GGGTCAAGGAGTGGACGGCGGAGGCCATTTTCCACCGGGC	
CCTTTACGAGCTTTCGGTGATAGAGCGCATGGGGTTTCCC	1800
GGCTACTTCTCATCGTCCAGGACTACATCAACTGGGCCC	
GGAGAAACGGCGTCTCCGTGGGGCCCCGGCAGGGGGAGCGC	
CGCCGGGAGCCTGGTGGCCTACGCCGTGGGGATCACCAAC	
ATTGACCCCTCCGCTTCGGCCTCCTCTTTGAGCGCTTCC	
TGAACCCGGAGAGGGTCTCCATGCCCGACATTGACACGGA	
CTTCTCCGACCGGGAGCGGGACCGGGTGATCCAGTACGTG	
CGGGAGCGCTACGGCGAGGACAAGGTGGCCCAGATCGGCA	
CCCTGGGAAGCCTCGCCTCCAAGGCCGCCCTCAAGGACGT	
GGCCCGGGTCTACGGCATCCCCACAAGAAGGCGGAGGAA	
TTGGCCAAGCTCATCCCGGTGCAGTTCGGGAAGCCCAAGC	
CCCTGCAGGAGGCCATCCAGGTGGTGCCGGAGCTTAGGGC	
GGAGATGGAGAAGGACCCCAAGGTGCGGGAGGTCTTCGAG	
GTGGCCATGCGCCTGGAGGGCCTGAACCGCCACGCCTCCG	
TCCACGCCCGCGGGGTGGTGATCGCCGCCGAGCCCCTCAC	
GGACCTCGTCCCCCTCATGCGCGACCAGGAAGGGCGGCCC	
GTCACCCAGTACGACATGGGGGCGGTGGAGGCCTTGGGGC	
TTTTGAAGATGGACTTTTGGGCCTCCGCACCCTCACCTT	

FIG. 16A

CCTGGACGAGGTCAAGCGCATCGTCAAGGCGTCCCAGGGG	1920
GTGGAGCTGGACTACGATGCCCTCCCCCTGGACGACCCCA	
AGACCTTCGCCCTCCTCTCCCGGGGGGAGACCAAGGGGGT	
CTTCCAGCTGGAGTCGGGGGGGATGACCGCCACGCTCCGC	2040
GGCCTCAAGCCGCGGCGCTTTGAGGACCTGATCGCCATCC	
TCTCCCTCTACCGCCCCGGGCCCATGGAGCACATCCCCAC	
CTACATCCGCCGCCACCACGGGCTGGAGCCCGTGAGCTAC	2160
AGCGAGTTTCCCCACGCCGAGAAGTACCTAAAGCCCATCC	
TGGACGAGACCTACGGCATCCCCGTCTACCAGGAGCAGAT	
CATGCAGATCGCCTCGGCCGTGGCGGGGTACTCCCTGGGC	2280
GAGGCGGACCTCCTGCGGCGGTCCATGGGCAAGAAGAAGG	
TGGAGGAGATGAAGTCCCACCGGGAGCGCTTCGTCCAGGG	
GGCCAAGGAAAGGGGCGTGCCCGAGGAGGAGCCAACCGC	2400
CTCTTTGACATGCTGGAGGCCTTCGCCAACTACGGCTTCA	
ACAAATCCCACGCTGCCGCCTACAGCCTCCTCTCCTACCA	
GACCGCTACGTGAAGGCCACTACCCCGTGAGTTTCATG	2520
GCCGCCCTCCTCTCCGTGGAGCGGCACGACTCCGACAAGG	
TGGCCGAGTACATCCGCGACGCCCGGGCCATGGGCATAGA	
GGTCCTTCCCCCGGACGTCAACCGCTCCGGGTTTGACTTC	2640
CTGGTCCAGGGCCGGCAGATCCTTTTCGGCCTCTCCGCGG	
TGAAGAACGTGGGCGAGGCGGCGGCGGAGGCCATTCTCCG	
GGAGCGGGAGCGGGGCGGCCCTACCGGAGCCTCGGCGAC	2760
TTCTCAAGCGGCTGGACGAGAAGGTGCTCAACAAGCGGA	
CCCTGGAGTCCCTCATCAAGGCGGGCGCCCTGGACGGCTT	
CGGGGAAAGGGCGCGGCTCCTCGCCTCCCTGGAAGGGCTC	2880
CTCAAGTGGGCGGCCGAGAACCGGGAGAAGGCCCGCTCGG	
GCATGATGGGCCTCTTCAGCGAAGTGAGGAGCCGCCTTT	
GGCCGAGGCCGCCCCCCCTGGACGAGATCACCCGGCTCCGC	3000
TACGAGAAGGAGGCCCTGGGGATCTACGTCTCCGGCCACC	
CCATCTTGCGGTACCCCGGGCTCCGGGAGACGGCCACCTG	
CACCCTGGAGGAGCTTCCCCACCTGGCCCGGGACCTGCCG	3120
CCCCGGTCTAGGGTCCCTCCTTGCCGGGATGGTGGAGGAGG	
TGGTGCGCAAGCCCACAAAGAGCGGCGGGATGATGGCCCG	
CTTCGTCTCTCCGACGAGACGGGGGCGCTTGAGGCGGTG	3240
GCATTGCGCCGGGCCTACGACCAGGTCTCCCCGAGGCTCA	
AGGAGGACACCCCCGTGCTCGTCCTCGCCGAGGTGGAGCG	
GGAGGAGGGGGGCGTGCGGGTGCTGGCCCAGGCCGTTTGG	3360
ACCTACGAGGAGCTGGAGCAGGTCCCCCGGGCCCTCGAGG	
TGGAGGTGGAGGCCTCCCTCCTGGACGACCGGGGGGTGGC	
CCACCTGAAAAGCCTCCTGGACGAGCACGCGGGGACCCTC	3480
CCCCTGTACGTCCGGGTCCAGGGCGCCTTCGGCGAGGCCC	
TCCTCGCCCTGAGGGAGGTGCGGGTGGGGGAGGAGGCTGT	
AGGCGGCCGCGTGTTCCGGGCCTACCTCCTGCCCCGACCG	3600
GGAGGTCTTCTCCAGGGCGGCCAGGCGGGGGAGGCCAG	
GAGGCGGTGCCCTTCTAGGGGGTGGGCCGTGAGACCTAGC	
GCCATCGTTCTCGCCGGGGGCAAGGAGGCCTGGGCCCGAC	3720
CCCTTTTGG	

FIG. 16B

MGRELRF	120
ALAMTDHGNLFGAVEFYKKATEMGIKPILGYEAYVAAESR	
FDRKRKGKLDGGYFHLTLLAKDFTGYQNLVRLASRAYLEG	
FYEKPRIDREILREHAEGLIALSGCLGAEIPQFILQDRLD	
LAEARLNEYLSIFKDRFFIEIQNHGLPEQKKVNEVLKEFA	
RKYGLGMVATNDGHYVRKEDARAHEVLLAIQSKSTLDDPG	240
ALALPCEEFYVKTPEEMRAMFPPEEEVGGRSPLTTPWRSPh	
VQGAAGTRWSTRIPRFPLPEGRTEAQYLMELTFKGLLR	
RYPDRITEGFYREVFRLSGKLPPHGDGEALAEALAQVERE	360
AWERLMKSLPPLAGVKEWTAEAI FHRALYELSAIERMGFP	
GLLPHRPGHLHQLGPEKGVSVGPGRGGAAGSLVAYAVGITN	
IDPLRFGLL FERFLNPERVSMPTDIDTDFSDRERDRVIQYV	480
RERYGEDKVAQIGTLGSLASKAALKEVARVYGI PRKKAEE	
LAKLIPVQFGKPKPLQEA IQVPELRAEMEKDPKVREVLE	
VAMRLEGLNRHASVHAGRGGVFSEPLTDLVPLCATRKGGP	600
YTQYDMGAVEALGLLKMDFLGLRTLTLFLDEVKRIVKASQG	
VELDYDALPLDDPKTFALLSRGETKGVFQLESGGMTATLR	
GLKPRRFEDLIAILSLYRPGPMEHIPTYIRRHHGLEPVSy	720
SEFPHAEKYLKPIIDETYGIPVYQEQIMQIASAVAGYSLG	
EADLLRRSMGKKKVEEMKSHRERFVQAKERGVPEEEANR	
LFDMLEAFANYGFNKSHAAAYSLLSYQTAYVKAHYPVFEFM	840
AALLSVERHDSKVAEYIRDARAMGIEVLPPDVNRS GFDF	
LVQGRQILFGLSAVKNVGEAAAEAILRERERGGPYRSLGD	
FLKRLDEKVLNKRRTLES LIKAGALDGFGERARLLASLEGL	960
LKWAAENREKARSGMMGLFSEVEEPPLAEAAPLDEITRLR	
YEKEALGIYVSGHPILRYPGLRETATCTLEELPHLARDLP	
PRSRVLLAGMVEEVVRKPTKSGGMMARFVLSDETGALEAV	1080
AFGRAYDQVSPRLKEDTPVLVLAEVEREEGGVVRVLAQAVW	
TYQELEQVPRALEVEVEASLPDDRGV AHLKSLLD EHAGTL	
PLYVRVQAFGEALLALREVRVGEELGALEAAGFPAYLL	1200
PNREVSPRLTGSGGPRGRALSTGLALKTYPIALPGGNEAL	
ARPLL	

FIG. 16C

	Start1	Start2	3'-Exo I
T.th.	VERVVRTLLDGRFLLEEGVGLNEWRYPPFLEGEAVVVLDTTGLAG-----LDEVIEVGLLRLEGG---RRLPF		
D.rad.		PWPQDVVVFDDLETTGFSPA-----SAAIVEIGAVRIVGGQIDETLKF	
Bac.sub.	HGIKMIYMEANLVDDGVPIAYNAHRLLLEEETVVVFDDVETTGLSAV-----YDTIIELAAVKVKGGE--IIDKF		
H.inf.		MINPNRQIVLDTTETTGMMNQLGHAHYEGHCIIIEIGAVELINRR-YTGNNX	
E.c.		MSTAITRQIVLDTTETTGMMNQIGAHSEGHKIIIEIGAVEVVNRR-LTGNNF	
H.pyl.	NLEYLKACGLNFIEETSENLTILKNLKTPLKDEVFSFIDLETTGSCPI-----KHEILEIGAVQVKGGE--IINRF		

	3'-Exo II
T.th.	QSLVR-PLPP---AARSWNLT---GIPREALEEAPSLEEVLEKAYPLRGDATLVIHNAAFDLGLFL-RPALEGLG
D.rad.	ETLVR-PTRPDGMSLIPWQAQRVHGIDEMVRRAPAXKDVLPDFDFVDGSAVVAHNVSFDGGFM-RAGAERLG
Bac.sub.	EAFAN-PHRP---LSATIIELT---GITDDMLQDAPDVVDVIRDFREWIGDDILVAHNASFDMGFL-NVAYKKLL
H.inf.	HIYIK-PDRP---XDPDAIKVH---GITDEMLADKPEFKEVAQDFLDYINGAELLIHNAFPDVGFM-DYEFRRKLN
E.c.	HVYLK-DRLV---DPEAFGVH---GIAVDFLLDKPTFAEVAVEFMDYIRGAELVHNAAFDVGFM-DYEFSLLK
H.pyl.	ETLVKVKSV-----DYIAELT---GITYEDTLNAPSAHEALQELRLFLGNSVFAHNANFDYNFLGRYFVEKLH

	3'-Exo IIIC
T.th.	-----YRLENPVVDSLRLARRGLPGLRRYGLDALSEVLELPRRT--CHRALEDVERTLAVVHEVYVYMLT-----SG
D.rad.	-----LSWAPERELCTMQLSRRAFPERRTHNLTVLAERLGLLEFAPGGRHRSYGDVQVTAQAYLRLLLELLG-----ER
Bac.sub.	E---VEKAKNPVIDTLELGRFLYPEFKNHRNLTLCKKFDIELTQ--HRAIYDTEATAYLLKMLKDAA-----EK
H.inf.	-LNVKTDDICLVDTLQMARQMPGKRN-NLDALCDRLGIDNSKRTLHGALLDAEILADVLYLMMTGGQTNLFDEEEE
E.c.	RDIAKTNTFCKVTDLSLAVARKMFPGKRN-SLDALCARYEIDNSKRTLHGALLDAQIILAEVYLAMTGGQTSMAFAME
H.pyl.	-----CPLLNLKLCTLDLSKRAILSMRY-SLSFLKELLGFGIEV--SHRAYADALASYKLFELICLINLP--SYIKT

FIG.17

FIG.18A

ATGGTGGAGCGGGTGGTGC GGACCCCTTCTGGACGGGAGGT 40
 TCCTCCTGGAGGAGGGGGTGGGGCTTTGGGAGTGGCGCTA
 CCCCTTTCCCCTGGAGGGGGAGGCGGTGGTGGTCCTGGAC 120
 CTGGAGACCACGGGGCTTGCCGGCCTGGACGAGGTGATTG
 AGGTGGGCCTCCTCCGCCTGGAGGGGGGGAGGCGCCTCCC 200
 CTTCCAGAGCCTCGTCCGGCCCCCTCCCGCCCGCCGAAGCC
 CGTTCGTGGAACCTCACCGGCATCCCCCGGGAGGCCCTGG 280
 AGGAGGCCCCCTCCCTGGAGGAGGTTCTGGAGAAGGCCTA
 CCCCTCCGCGGCGACGCCACCTTGGTGATCCACAACGCC 360
 GCCTTTGACCTGGGCTTCCTCCGCCCGGCCTTGGAGGGCC
 TGGGCTACCGCCTGGAAAACCCCGTGGTGGACTCCCTGCG 440
 CTTGGCCAGACGGGGCTTACCAGGCCTTAGGCGCTACGGC
 CTGGACGCCCTCTCCGAGGTCTTGGAGCTTCCCCGAAGGA 520
 CCTGCCACCGGGCCCTCGAGGACGTGGAGCGCACCCCTCGC
 CGTGGTGCACGAGGTATACTATATGCTTACGTCCGGCCGT 600
 CCCCCGACGCTTTGGGAACTCGGGAGGTAG

MVERVVRTLLDGRFLLEEGVGLWEWRYPFPLEGEAVVVD 40
 LETTGLAGLDEVIEVGLLRLEGGRRLPFQSLVRPLPPAEA
 RSWNLTGIPREALEEAPSLEEVLEKAYPLRGDATALVIHNA 120
 AFDLGFLRPALEGLGYRLNPVVD SLRLARRGLPGLRRYG
 LDALSEVLELPRRTCHRALEDVERTLAVVHEVYYMLTSGR 200
 PRTLWELGRZ

FIG.18B

Alignment of dnaA genes.

P. mar.	MLEASWEK	VQSSL--KQNLK--	-----PSYE	TWIRTEFSG--FKN	GELTLIAPNSFSSAW	LKNYSQTIQETAE-	65
Syn. sp.	MVSCENLWQQ	ALAIL--ATQLTK--	-----PAFD	TWIKASVLIS--LGD	GVATIQVENGFVLAH	LQKSYGPLIMEVLT-	67
B. sut.	MENILDLNQ	ALAI--EKKLSK--	-----PSFE	TWIKSTKAHS--LQG	DTLTITAPNEFARDW	LESRYLHLIADTIY-	67
M. tub.	MTDDPGSGFTTVNA	WSELNGDKVDDGP	SSDANLSAFLTPQOR	AMLNLVQPLT--IVE	GFALLSVPSFFVQNE	IERRHRAPIITDALS-	87
T. th.	MSHEAVWQH	VLEHI--RRSITE--	-----VEFH	TWFERIRPLG--IRD	GVLELAVPTSFALDW	IRRHVAGLIQEGPR-	66
E. coli	MSLSLWQQ	CLARL--QDELPA--	-----TEFS	MWIRPLQAE--LSD	NTLALYAPNRFVLDW	VRDKYLNININGLLT-	64
T. mar.	MKER	ILQEI--KTRVNR--	-----KSWE	LWFSFDVKS--IBG	NKVVSFVGNLFIREW	LEKKYYSVLSKAVK-	61
H. pyl.	MDTNANNIEKE	ILALVKQNPKVSL--	-----IEYE	NYFSQLKYNPNASKS	DIAFFYAENQVLCCT	ITARYGALLKEILSQ	72
P. mar.	EIFG---	EPVTVHVK	VKANAESSDEHYSSA	P-----	ITPPLEASPGSV	DSSGSSLRLSK	130
Syn. sp.	DLTG---	QEITVKLI	TDGLEPHS---	LIGQ	E-----	SSLPMETTP	115
B. sut.	ELTG---	EELSIFV	IPQNDVEDFMPKPQ	VKAVKEDTSDFPQN	-----	-----	119
M. tub.	RRLGH-QIQGVRLA	PPATDEADDTTVPPS	ENPATSPDITTTDND	EIDDSAAARGDNQHS	WPSYFTEPHNTDSA	TAGVTSLNRRYTFTD	176
T. th.	LLGAQ-APRFELRV	PGVVQEDIFQPPPS	PPAQAP-----	-----	-----	-----	108
E. coli	SFCGADAPQLRFEVG	TKPVTQTPQAAVTSN	VAAPAQVAQTQORA	APSTRSGWNVPA	EP-----	-----	140
T. mar.	VVLG---	NDATFEIT	YEAFEPHSSYSEPLV	KKRAVLITP-----	-----	-----	106
H. pyl.	NKVG-MHLAHSVDVR	IEVAPKIQINAQSN	NYKAITS-----	-----	-----	-----	118
P. mar.	FVVGPNRMAHAAAM	AVAESPGREENPLFI	CGGVGLGKTHLMQAI	GHYRLEIDPGAKVSY	VSTETFTNDLIL--A	IRQDRMQAFDRYR-	217
Syn. sp.	FVVGPTNRMAHAASL	AVAESPGREENPLFL	CGGVGLGKTHLMQAI	AHYRLEMYPAKVVY	VSTERFTNDLIT--A	IRQDNMEDFRSYR-	202
B. sut.	FVIGSGNRFAHAASL	AVAEPAPAKAVNPLFI	YGGVGLGKTHLMHAI	GHYVIDHNPSPAKVVY	LSSEKFTINEFIN--S	IRDNKAVDFRNRYR-	206
M. tub.	FVIGASNRFAHAAL	AIAPAPARAVNPLFI	WGESGLGKTHLLHAA	GNVAQRLFGMRVKY	VSTEEFTNDFIN--S	LRDDRKVAFKRSYR-	263
T. th.	SWGPTTPWPHGGAV	AVAESPGRAVNPLFI	YGGRGKTKTYLMHAV	GPLRAKRFPHMRLEY	VSTETFINELINRPS	AR-DRMTEFRERYR-	196
E. coli	FVEGKSNQLARAAAR	QVADNPGGAYNPLFL	YGGTGLGKTHLLHAV	GNGIDARKPNKVVY	MHSERFVQDMVK--A	LQNNALIEEFKRYR-	227
T. mar.	FVVGPGNSFAYHAAL	EVAKHPR-YNPLFI	YGGVGLGKTHLLQSI	GNVYVQNEPDLRVMY	ITSEKFTNDLVD--S	MKEGKLINEFREKYR	193
H. pyl.	FVVGSCNNTVVEIAK	KVAQSDTPPPYNPLVF	YGGTGLGKTHILNAI	GNHALEK--HKKVV	VTSEDFLTDFLK--H	LDNKTMDSFKAKYR-	203

FIG.19A

P. mar.	AADLLVDDIQFIEG	KEYTQEEFFHTFNAL	HDAGSQIVLASDRPP	SQIPRIQERLMSRFS	MGLIADVQAPDLETR	MAILQKKAHERVGL	307
Syn. sp.	SADFLIDDIOFIKG	KEYTQEEFFHTFNAL	HEAGKQVWASDRAP	QRIPGIQDRILSRFS	MGLIADIOVPDLETR	MAILQKKAHYDRIRL	292
B. sut.	NVDVLLIDDIOFLAG	KEQTQEEFFHTFNAL	HEESKQIVISSDRPP	KEIPTLEDRLSRFS	WGLITDITPPDLETR	IAILRKKAKAEGLDI	296
M. tub.	DVDVLLVDDIQFIEG	KEGIQEEFFHTFNAL	HNANKQIVISSDRPP	KQLATLEDRLSRFS	WGLITDVOPPELETR	IAILRKKAKAERLAV	353
T. th.	SVDLLLVDDVQFIAG	KERTQEEFFHTFNAL	YEAHKQIILSSDRPP	KDILITLRLSRFS	WGLITDNPAPDLETR	IAILKMNAS-SGPED	285
E. coli	SVDALLIDDIOFFAN	KERSQEEFFHTFNAL	LEGNOQIILTSDRYP	KEINGVEDRLKSFRG	WGLIVAJEPPPELETR	VAILMKKADENDIRL	317
T. mar.	KVDILLIDDVQFLIG	KTGVQTELFTFNEL	HDSGKQIVICSDREP	QKLSEFQDRLVSRFQ	MGLIVAKLEPPDETR	KSIARKMLEIEHGEL	283
H. pyl.	HCDFLLDDAQFLOQ	KPKLEEEFFHTFNEL	HANSKQIVLISDRSP	KNLAGLEDRLKSFRF	WGITAKVMPDLETK	LSIVKQKCOLNQITL	293

P. mar.	PRDLIQFIAGRFTSN	IRELEGALTRAIAFA	SITGLPMTVDSIAPM	LD-----PNGQVEVT	PKQVLDKVAEVFKVT	PDEMSASRRR-FVS	392
Syn. sp.	PKEVIEYIASHYTSN	IRELEGALIRALAYT	SLSNVAMTVENIAPV	LN-----PPVEKVAAA	PETITITIVAQHYQLK	VEELLSNSRRR-EVS	377
B. sut.	PNEVMLYLANQIDSN	IRELEGALIRVWAYS	SLINKDINADLAAEA	LKOII-PSSKPKVIT	IKEIQRVVGOQFNK	LEDFKAKKRTK-SVA	384
M. tub.	PDDVLELFIASSIERN	IRELEGALIRVTAF	SINKTPIDKALAEIV	LRDLI-ADANTMOIS	AATIMAATAEYFDTT	VEELRGPGKTR-ALA	441
T. th.	PEDALEYIARQVTSN	IREWEGALMRASPFA	SINGVELTRAVAAKA	LRHLR-P--RELEAD	PLEIRKAAGPVPRPE	TPGGAHGERRKKEVV	372
E. coli	PGEVAFFIAKRLRSN	VRELEGALNRVIANA	NFTGRAITIDFVREA	LRDLL-A-LQEKLV	IDNIQKTVAEYTKIK	VADLLSKRRSR-SVA	404
T. mar.	PEEVLFNFVAENVDDN	LRRLRGAIKLLVYK	ETTCKEVDLKEAILL	LKDFIKPNRVKAMD	IDELIEIVAKVTGVP	REEILSNSRNV-KAL	372
H. pyl.	PEEVMEYIAQHISDN	IRQMEGAIKISVNA	NLMNASIDLNLAKTV	LEDL--QKDHAEGSS	LENILLAVAQSLNLK	SSEIKVSSRQK-NVA	380

P. mar.	QARQVGYLMRQGTN	LSLPRIGDTFGGKDH	TTVMAIEQVEKKLS	S-----DPQIA	SOVQKIRDLLOIDSR	RKR----	461
Syn. sp.	LARQVGYLMRQHTD	LSLPRIGEAFGGKDH	TTVMYSCDKITQLQQ	K-----DMETS	QTLTSLSHRINIAGQ	APES----	447
B. sut.	FPRQIAMYL SREMTD	SSLPKIGEFGGRDH	TTVTHAHEKISKLLA	D-----DEQLQ	QHVKEIKEQLK----	-----	446
M. tub.	QSRQIAMYL CRELTD	LSLPKIGQAFG-RDH	TTVMAQRKILSEMA	E-----RREVF	DHVKELTTRIRQSRK	R-----	507
T. th.	LPRQIAMYL VRELTP	ASLPEIGQLFGGRDH	TTVRYAIQKVQELAG	KP-----DREVQ	GLLRTLREACTDPVD	NLMTTCG	446
E. coli	RPRQAMALAKELTN	HSLPEIGDAFGGRDH	TTVLHACRKIEQLRE	E-----SHDIK	EDFSNLIRTLSS----	-----	467
T. mar.	TARRIGMVVAKNYLK	SSLRTIAEFN-RSH	PVVVDSVKVKDSLL	KG-----NKQLK	ALIDEVIGEISRRAL	SG-----	440
H. pyl.	LARKLVVVFARLYTP	NPTLSLAQFLDLKDH	SSISKMYSGVKGMLE	EESKSPFVLSLREEIK	NRLNELNDKKTAFNS	SE-----	457

FIG. 19B

GTGTCGCACGAGGCCGTCTGGCAACACGTTCTGGAGCA⁻CA
 TCCGCCGCAGCATCACCGAGGTGGAGTTCCACACCTGGTT
 TGAAAGGATCCGCCCCCTTGGGGATCCGGGACGGGGTGCTG 120
 GAGCTCGCCGTGCCCACCTCCTTTGCCCTGGACTGGATCC
 GGCGCCACTACGCCGGCCTCATCCAGGAGGGCCCTCGGCT
 CCTCGGGGCCCAGGCGCCCCGGTTTGAGCTCCGGGTGGTG 240
 CCCGGGGTCTAGTCCAGGAGGACATCTTCCAGCCCCCGC
 CGAGCCCCCGGCCCAAGCTCAACCCGAAGATACCTTTAA
 AACTTCGTGGTGGGGCCCAACAACCTCCATGGCCCCACGGC 360
 GGCGCCGTGGCCGTGGCCGAGTCCCCCGGCCGGGCGCTACA
 ACCCCCTCTTCATCTACGGGGGCGGTGGCCTGGGAAAGAC
 CTACCTGATGCACGCCGTGGGCCCCTCCGTGCGAAGCGC 480
 TTCCCCCACATGAGATTAGAGTACGTTTCCACGGAAACTT
 TCACCAACGAGCTCATCAACCGGCCATCCGCGAGGGACCG
 - GATGACGGAGTTCCGGGAGCGGTACCGCTCCGTGGACCTC 600
 CTGCTGGTGGACGACGTCCAGTTCATCGCCGGAAAGGAGC
 GCACCCAGGAGGAGTTTTTCCACACCTTCAACGCCCTTTA
 CGAGGCCCACAAGCAGATCATCCTCTCCTCCGACCGGCCG 720
 CCAAGGACATCCTCACCTTGGAGGCGCGCCTGCGGAGCC
 GCTTTGAGTGGGGCCTGATCACCGACAATCCAGCCCCCGA
 CCTGGAAACCCGGATCGCCATCCTGAAGATGAACGCCAGC 840
 AGCGGGCCTGAGGATCCCGAGGACGCCCTGGAGTACATCG
 CCCGGCAGGTCACCTCCAACATCCGGGAGTGGGAAGGGGC
 CCTCATGCGGGCATCGCCTTTCGCCTCCCTCAACGGCGTT 960
 GAGCTGACCCGCGCCGTGGCGGCCAAGGCTCTCCGACATC
 TTCGCCCCAGGGAGCTGGAGGCGGACCCCTTGGAGATCAT
 CCGCAAAGCGGCGGGACCAGTTCGGCCTGAAACCCCGGGA 1080
 GGAGCTCACGGGGAGCGCCGCAAGAAGGAGGTGGTCCTCC
 CCCGGCAGCTCGCCATGTACCTGGTGCGGGAGCTCACCCC
 GGCTTCCCTGCCCGAGATCGACCAGCTCAACGACGACCGG 1200
 GACCACACCACGGTCCTCTACGCCATCCAGAAGGTCCAGG
 AGCTCGCGGAAAGCGACCGGGAGGTGCAGGGCCTCCTCCG
 CACCCTCCGGGAGGCGTGACATGA

FIG.20A

VSHEAVWQHVLHIRRSITEVEFHTWFERIRPLGIRDGVL
ELAVPTSFALDWIRRHYAGLIQEGPRLPGAQAPRFELRVV
PGVVQEDIFQPPSPPAQAQPEDTFKTSWWGPTTPWPHG 120
GAVAVAESPGRAYNPLFIYGGRGLGKTYLMHAVGPLRAKR
FPHMRLEYVSTETFTNELINRPSARDRMTEFRERYRSVDL
LLVDDVQFIAGKERTQEEFFHTFNALYEAHKQIILSSDRP 240
PKDILTLEARLRSRFEWGLITDNPAPDLETRIAILKMNAS
SGPEDPEDALEYIARQVTSNIREWEGALMRASPFASLNGV
ELTRA VAAKALRHLPRELEADPLEIIRKAAGPVRPETPG 360
GAHGERRKKEVVLPRQLAMYLVLRELTPASLPEIDQLNDDR
DHTTVLYAIQKVQELAESDREVQGLLRTLREACT

FIG.20B

ATGAACATAACGGTTCCCAAAAACTCCTCTCGGACCAGC 40
 TTTCCTCCTGGAGCGCATCGTCCCCTCTAGAAGCGCCAA
 CCCCTCTACACCTACCTGGGGCTTTACGCCGAGGAAGGG 120
 GCCTTGATCCTCTTCGGGACCAACGGGGAGGTGGACCTCG
 AGGTCCGCCTCCCCGCCGAGGCCCAAAGCCTTCCCCGGGT 200
 GCTCGTCCCCGCCAGCCCTTCTTCCAGCTGGTGCGGAGC
 CTTCTGGGGACCTCGTGGCCCTCGGCCTCGCCTCGGAGC 280
 CGGGCCAGGGGGGGCAGCTGGAGCTCTCCTCCGGGCGTTT
 CCGCACCCGGCTCAGCCTGGCCCCCTGCCGAGGGCTACCCC 360
 GAGCTTCTGGTGCCCCGAGGGGGAGGACAAGGGGGCCTTCC
 CCTCCGGACGCGGATGCCCTCCGGGGAGCTCGTCAAGGC 440
 CTTGACCCACGTGCGCTACGCCGCGAGCAACGAGGAGTAC
 CGGGCCATCTTCCGCGGGGTGCAGCTGGAGTTCTCCCCC 520
 AGGGCTTCCGGGCGGTGGCCTCCGACGGGTACCGCCTCGE
 CCTCTACGACCTGCCCCCTGCCCAAGGGTTCCAGGCCAAG 600
 GCCGTGGTCCCCGCCCGGAGCGTGACGAGATGGTGCGGG
 TCCTGAAGGGGGCGGACGGGGCCGAGGCCGTCTCGCCCT 680
 GGGCGAGGGGGTGTGGCCCTGGCCCTCGAGGGCGGAAGC
 GGGGTCCGGATGGCCCTCCGCCTCATGGAAGGGGAGTTCC 760
 CCGACTACCAGAGGGTCATCCCCCAGGAGTTCGCCCTCAA
 GGTCCAGGTGGAGGGGGAGGCCCTCAGGGAGGCGGTGCGC 840
 CGGGTGAGCGTCTCTCCGACCGGCAGAACCACCGGGTGG
 ACCTCCTTTTGGAGGAAGGCCGGATCCTCCTCTCCGCCGA 920
 GGGGGACTACGGCAAGGGGCAGGAGGAGGTGCCCCGCCAG
 GTGGAGGGGCCGGACATGGCCGTGGCCTACAACGCCCGCT 1000
 ACCTCCTCGAGGCCCTCGCCCCCGTGGGGGACCGGGCCCA
 CCTGGGCATCTCCGGGCCCACGAGCCCGAGCCTCATCTGG 1080
 GGGGACGGGGAGGGGTACCGGGCGGTGGTGGTGCCCCCTCA
 GGGTCTAG 1128

FIG.21A

MNITVPPKLLSDQLSLLERIVPSRSANPLYTYLGLYAEEG 40
ALILFGTNGEVDLEVRLPAEAQSLPRVLVPAQPFFQLVRS
LPGDLVALGLASEPGQGQLELSSGRFRTRLAPAEGLYP 120
- ELLVPEGEDKGAFPLRTRMPSELVKALTHVRYAASNEEY
RAIFRGVQLEFSPQGFRAVASDGYRLALYDLPLPQGFQAK 200
AVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALEGGS
GVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVR 280
RVSVLSDRQNHVRVDLLLEEGRIILSAEGDYGKGQEEVPAQ
VEGPDMAVAYNARYLLEALAPVGDRHLGISGPTSPSLIW 360
GDGEGYRAVVVPLRVZ

FIG.21B

T. th. beta	MNITVPKLLSDQLSLLERIVPSRSANPLYTYLGLYAEAGALILFGTNGEVDLEVRLPAE
E. coli. bet	MKFTVEREHLKPLQOVSGPLGGRPTLPILGNLLIQVADGTLSTGTDLMEMVARVALV
P. mirab. be	MKFIIEREQLLKPLQOVSGPLGGRPTLPILGNLLKVTENTLSLTGTDLEMEMMARVSL
H. infl. bet	MQFSISRENLLKPLQOVCGVLSNRPNIPVIANVLLQIEDYRLTTGTDLLEVELSSQTQLS
P. put. beta	MHFTIQREALKPLQVAGVVERRQTLPVLSNVLVWQGOQLSLTGTDLLEVELVGRVQLE
B. cap. beta	MKFTIQNDILAKNLKKITRVLVKNISFPILENILIQVEDGTLSTTTNLEIELISKIEII
	* * * * *
T. th. beta	AQSLP-RVLVPAQFFQLVRSPLPGDLVALGLASEPGQGQLELSSGRFRTRLSLAPAEY
E. coli. bet	QPHEPGATTVPARKFFDICRGLP-EGAEIAVQLE---GERMLVRSGRSRSFSLSTLPAADF
P. mirab. be	QSHGIGATTVPARKFFDIWRGLP-EGAEISVELD---GDRLLVRSGRSRSFSLSTLPAADF
H. infl. bet	SSSENGFTTIPAKKFLDICRTLS-DDSEITVTFE---QDRALVQSGRSRFTLATQPAEY
P. put. beta	EPAEPGEITVPARKIMDICKSLP-NDALIDIKVD---EQKLLVKAGRSRFTLSTLPANDE
B. cap. beta	TKYIPGKTTISGRKIILNICRTLS-EKSKIRMQLK---NKKMYISSENSNYILSTLSADTF
	* * * * *
T. th. beta	PELLVPEGEDKGAFFLTRMPSGELVKALTHVRYAASNEEYRAIFRGVQLEFSPQGFRV
E. coli. bet	PNLDD--WQSEVEFTLPQAT----MKRLIEATQFSMAHQDVRYIYNGMLFETEGEELRTV
P. mirab. be	PNLDD--WQSEVEFTLPQAT----LKRLIESTQFSMAHQDVRYIYNGMLFETENTELRTV
H. infl. bet	PNLTD--WQSEVDFELPQNT----LRRLIEATQFSMAHQDARYFLNGMKFETEGNLLRTV
P. put. beta	PTVEE--GPGSLTCNLEQSK----LRRLIERTSFAMAQQDVRYIYNGMLLEVSRNTLRV
B. cap. beta	PNHQN--FDYISKFDISSNI----LKEMIEKTEFSMGKQDVRYIYNGMLLEKDKFLRSV
	* * * * *
T. th. beta	ASDGYRLALYDLPLPQGFQA--KAVVPARSVDEMVRVLKGADGAELALGEGVLALALE
E. coli. bet	ATDGHRLAVCSMPIGQSLPS-HSVTVPRKGVTELMRLDGC-GDNPLRVQIGSNIRAHVG
P. mirab. be	ATDGHRLAVCAMDIGQSLPG-HSVTVPRKGVTELMRLLDGSGESLQLQIGSNIRAHVG
H. infl. bet	ATDGHRLAVCTISLEQELQN-HSVILPRKGVLELVRLET-NDEPARLQIGTNNLRVHTK
P. put. beta	STDGHRLALCSMSAPIEQEDRHQVIVPRKGILELARLLTD-PEGMVSIVLGQHHIRATTG
B. cap. beta	ATDGYRLAISYTLKKDINF-FSIIIPKAVMELLKLLNT-QPQLNILIGSNSIRIYTK
	** *** * * * *

FIG. 22A

T.th.beta	GGSGVRMALRIMEGEFPDYQRVTPQEFALKVQVEGEALREAVRRVSVLSRONHRVDLLL
E.coli.bet	---DFIFTSKLVNDRFPDYRRVLPKNPDKHLKAGCDLLKQAFARAAILSNEKFRGVRLYV
P.mirab.be	---DFIFTSKLVNDRFPDYRRVLPKNPTKTIVAGCDILKQAFSRAAILSNEKFRGVRINL
H.infl.bet	---NTVFTSKLIDGRFPDYRRVLPKNATKIVEGNWEMLKQAFARASILSNERARSVRLSL
P.put.beta	---EFFTSKLVNDRFPDYRRVLPKGGDKLVNDRQALREAFSRTAILSNEKYRGIRLQL
B.cap.beta	---NLIFTTQLIEGEYPDYKSVLFKEKNPIITNSILLKKSLLRVAILAHEKFCGIEIKI

*** * * *

T.th.beta	EEGRILLSAEGDYK-GQEEVPAQVEGPDMAVAYNARYLLEALAPVG-DRAHLGISGPTS
E.coli.bet	SENQLKITANNPEQEEAEIILDVTSYGAEMEIGFNVSYLVDVNLALKCENVRMMLTDSVS
P.mirab.be	TNGQLKITANNPEQEEAEITDVQYQGEEMEIGFNVSYLVDVNLTKCEEVKLLITDAVS
H.infl.bet	KENQLKITASNTEHEEAEIIVNNGEELEVGFNVTYILDVNLALKCNQVRMCLTDAFS
P.put.beta	AAGQLKITANNPEQEEAEIISVDVESSLEIGFNVSYLVDVNGVMTTEQVRLLILSDSNS
B.cap.beta	ENGKFKVLSDNQEEETAEDLFEIDYFGEKIEISINVYLLDVNNIKSENIALFLANKSKS

. * * * *

T.th.beta	PSLIWGDG-EGYRAVWVPLRVZ	(ID#108)
E.coli.bet	SVQIEDAASQSAAYVVMFMR LZ	(ID#109)
P.mirab.be	SVQVENVASAAAAAYVVMFMR L-	(ID#110)
H.infl.bet	SCLIENCEDSSCEYVIMPMRL-	(ID#111)
P.put.beta	SALLOEAGNDSSYVVMFMR L-	(ID#112)
B.cap.beta	SIQIEAENSSNAYVVMILKR-	(ID#113)

*

FIG.22B

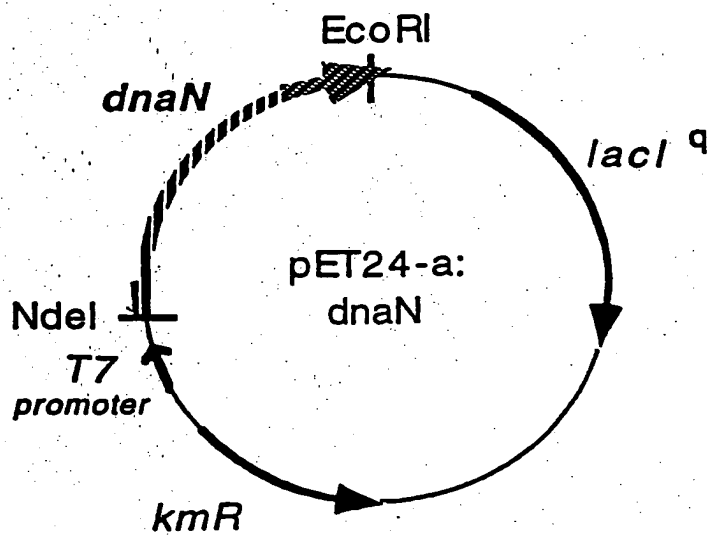
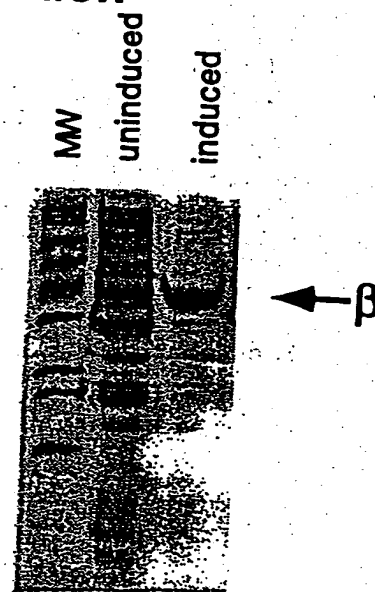


FIG.23

FIG.24A Induction



↓
Lysis
↓
Heat Step
↓

FIG.24B MonoQ Column

Fraction: 5 7 9 11 13 15 17 19 21 23 25

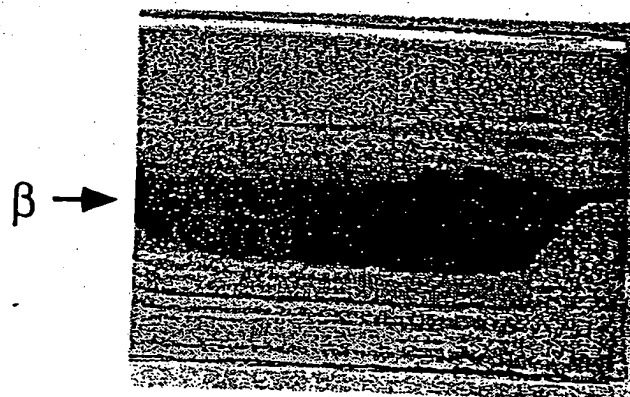


FIG.25A

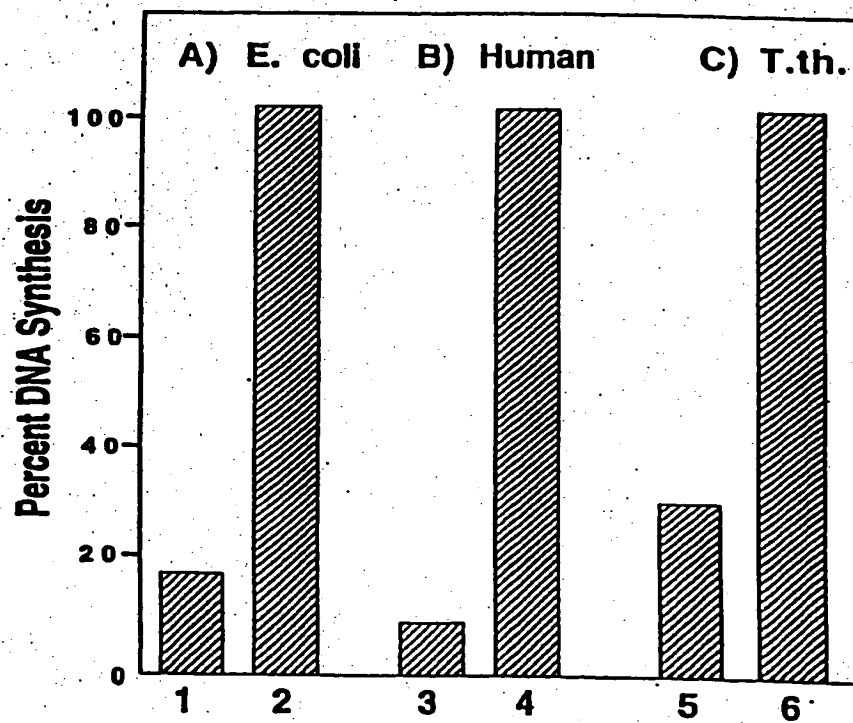
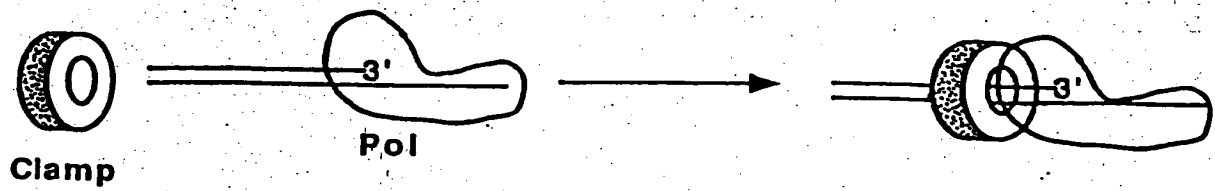


FIG.25B

FIG.26A

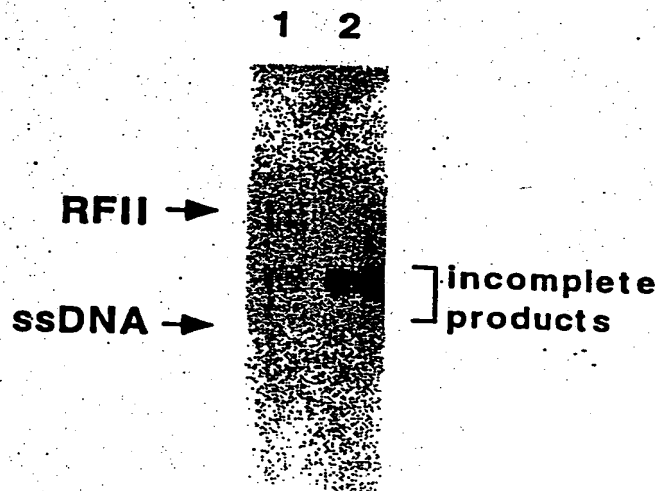
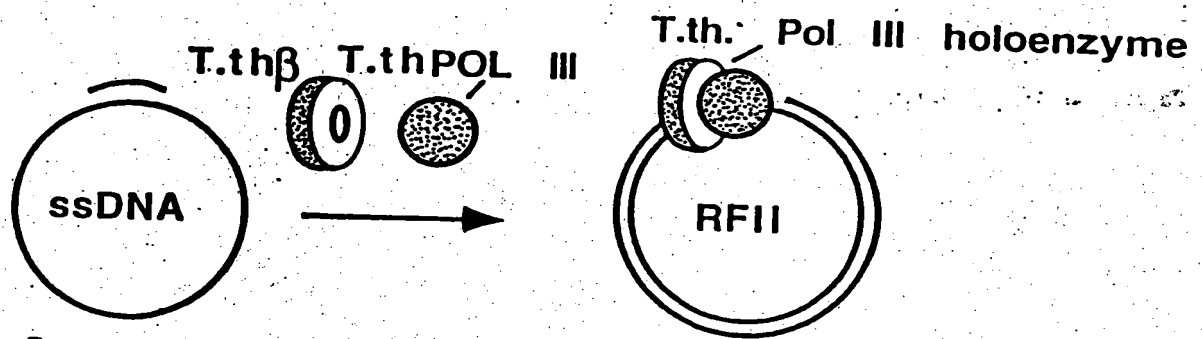


FIG.26B

α τ δ δ' SSB ϵ



FIG. 27

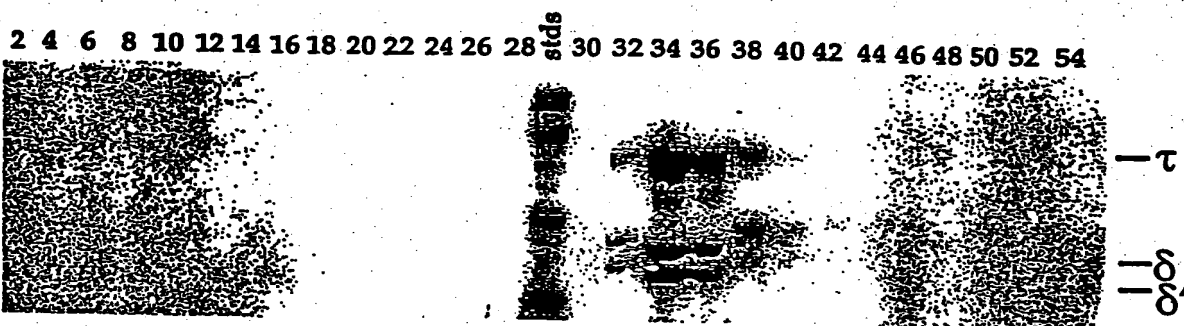


FIG. 28

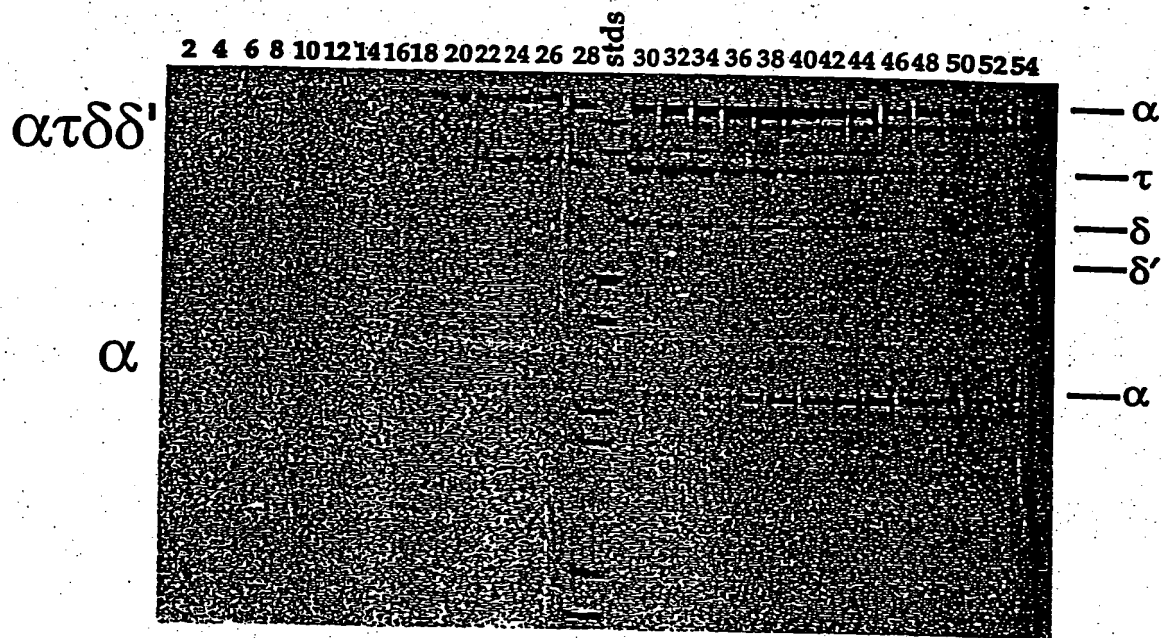


FIG. 29

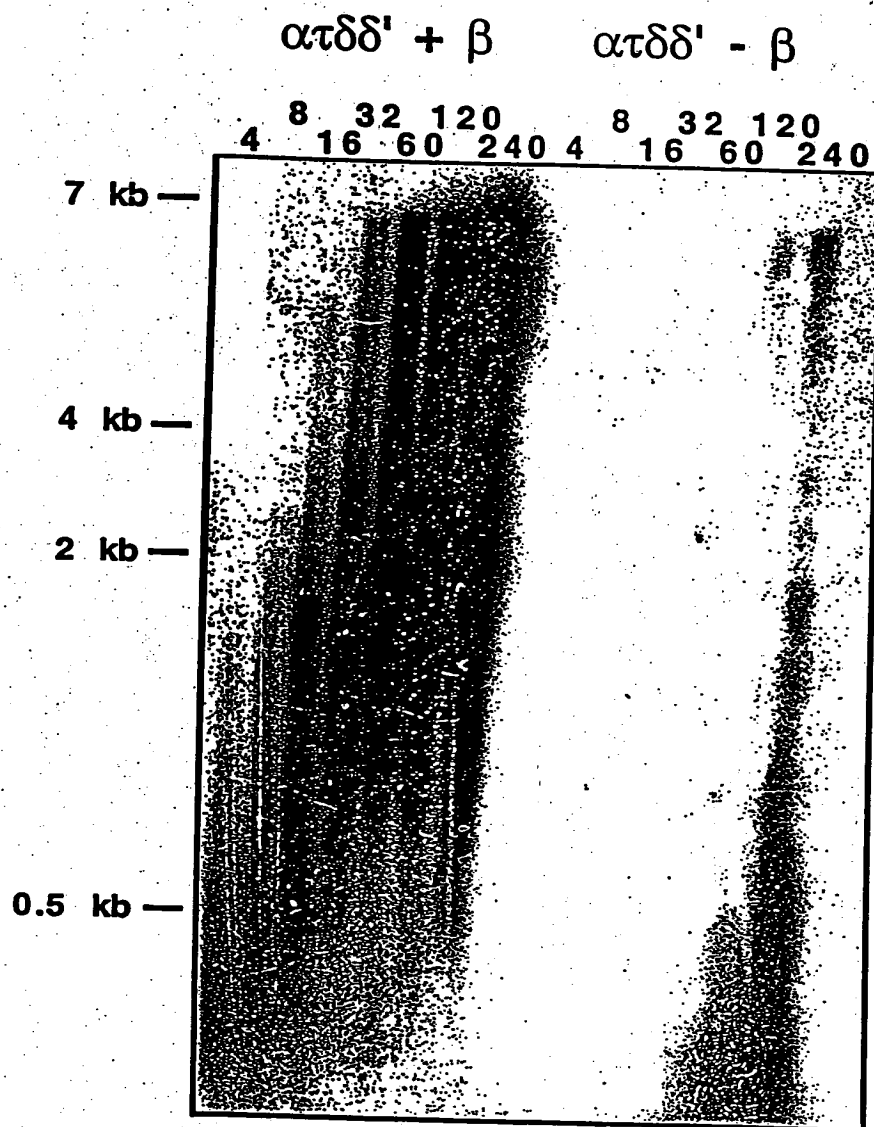


FIG. 30

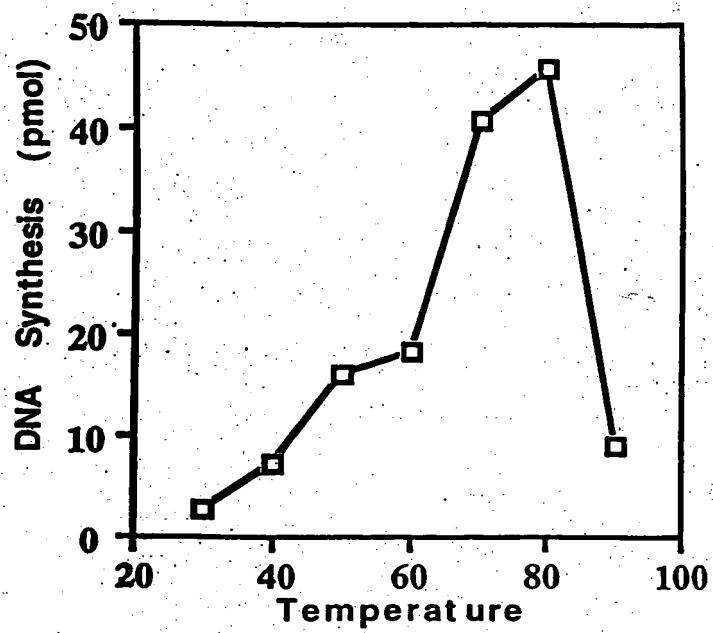


FIG. 31

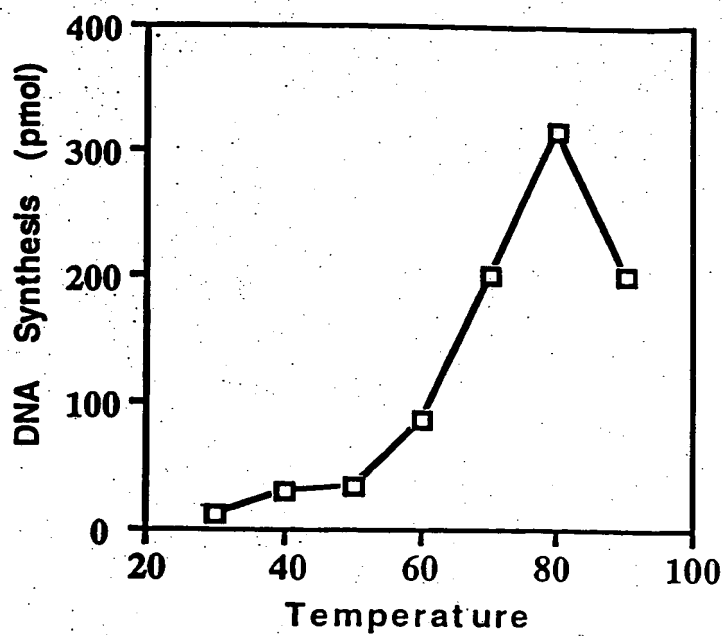


FIG. 32

α

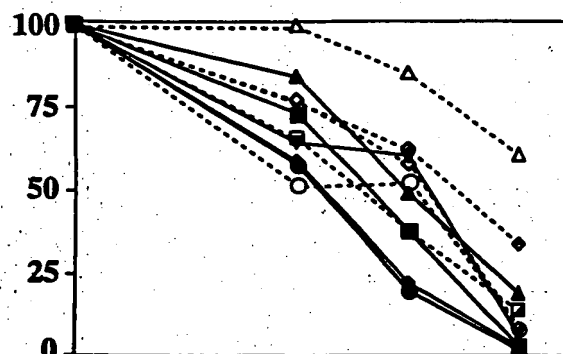


FIG. 33A

β

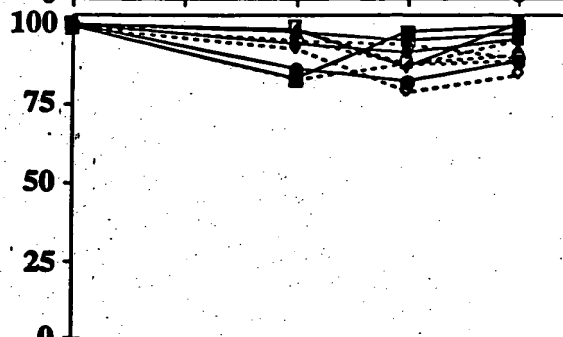


FIG. 33B

$\tau\delta\delta'$

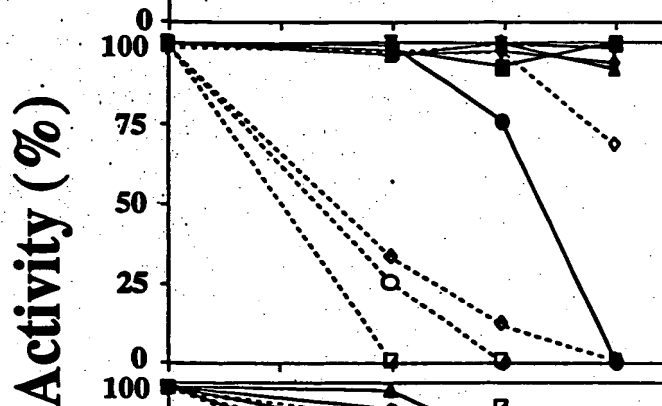


FIG. 33C

SSB

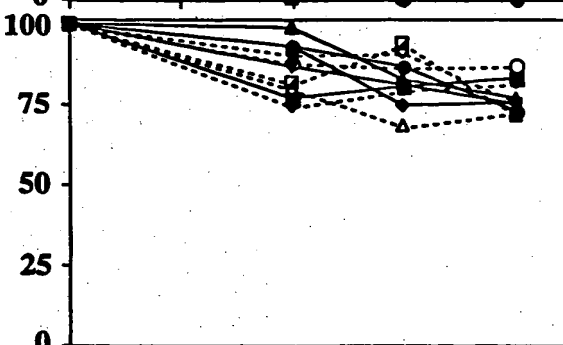


FIG. 33D

Pol III*

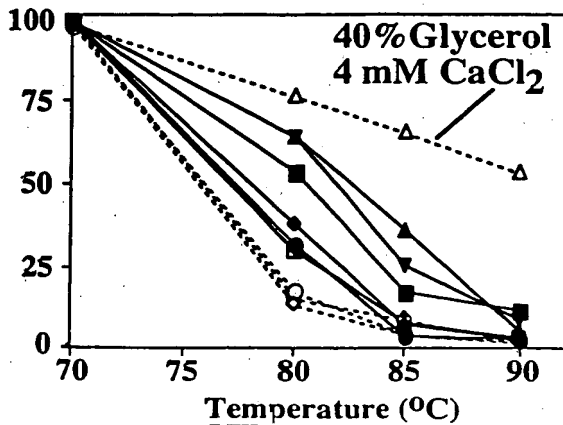


FIG. 33E

ATGAGTAAGGATTTTCGTCCACCTTCACCTGCACACCCAGTTCTCACTCCT	
GGACGGGGCTATAAAGATAGACGAGCTCGTGAAAAAGGCAAAGGAGTATG	100
GATACAAAGCTGTCGGAATGTCAGACCACGGAAACCTCTTCGGTTCGTAT	
AAATTCTACAAAGCCCCTGAAGGCGGAAGGAATTAAGCCCATAATCGGCAT	200
GGAAGCCTACTTTTACCACGGGTTCGAGGTTTGACAGAAAGACTAAAACGA	
GCGAGGACAACATAACCGACAAGTACAACCACCACCTCATACTTATAGCA	300
AAGGACGAAAAGGTCTAAAGAACTTAATGAAGCTCTCAACCCTCGCCTAC	
AAAGAAGGTTTTTTACTACAAACCCAGAATTGATTACGAACTCCTTGAAAA	400
GTACGGGGAGGGCCTAATAGCCCTTACCGCATGCCTGAAAGGTGTTCCCA	
CCTACTACGCTTCTATAAACGAAGTGAAAAAGGCGGAGGAATGGGTAAAG	500
AAGTTCAAGGATATATTTCGGAGATGACCTTTATTTAGAACTTCAAGCGAA	
CAACATTCAGAACAGGAAGTGGCAAACAGGAACCTTAATAGAGATAGCCA	600
AAAAGTACGATGTGAAACTCATAGCGACGCAGGACGCCCCACTACCTCAAT	
CCCGAAGACAGGTACGCCCACACGGTTCTTATGGCACTTCAAATGAAAAA	700
GACCATTACGAACTGAGTTCGGGAAACTTCAAGTGTTCAAACGAAGACC	
TTCACTTTGCTCCACCCGAGTACATGTGGAAAAAGTTTGAAGGTAAGTTC	800
GAAGGCTGGGAAAAGGCACTCCTGAACACTCTCGAGGTAATGGAAAAGAC	
AGCGGACAGCTTTGAGATATTTGAAAACCTCCACCTACCTCCTTCCCAAGT	900
ACGACGTTCCGCCCGACAAAACCCCTTGAGGAATACCTCAGAGAACTCGCG	
TACAAAGGTTTAAAGACAGAGGATAGAAAGGGGACAAGCTAAGGATACTAA	1000
AGAGTACTGGGAGAGGCTCGAGTACGAACTGGAAGTTATAAACAAAATGG	
GCTTTGCGGGATACTTCTTGATAGTTTCAAGACTTCATAAACTGGGCTAAG	1100
AAAAACGACATACCTGTTGGACCCGGAAGGGGAAGTGCTGGAGGTTCCCT	
CGTCGCATACGCCATCGGAATAACGGACGTTGACCCTATAAAGCACGGAT	1200
TCCTTTTTTGAGAGGTTCTTAAACCCCGAAAGGGTTTCCATGCCGGATATA	
GACGTGGATTTCTGTGAGGACAACAGGGAAAAGGTCATAGAGTACGTAAG	1300
GAACAAGTACGGACACGACAACGTAGCTCAGATAATCACCTACAACGTAA	
TGAAGGCGAAGCAAACACTGAGAGACGTGCAAGGGCCATGGGACTCCCC	1400
TACTCCACCGCGGACAAACTCGCAAAACTCATTCTCAGGGGGACGTTCA	
GGGAACGTGGCTCAGTCTGGAAGAGATGTACAAAACGCCTGTGGAGGAAC	1500
TCCTTCAGAAGTACGGAGAACACAGAACGGACATAGAGGACAACGTAAAG	
AAGTTCAGACAGATATGCGAAGAAAGTCCGGAGATAAAACAGCTCGTTGA	1600
GACGGCCCTGAAGCTTGAAGGTCTCACGAGACACACCTCCCTCCACGCCG	
CGGGAGTGGTTATAGCACCAAAGCCCTTGAGCGAGCTCGTTCCCCTCTAC	1700
TACGATAAAGAGGGCGAAGTCGCAACCCAGTACGACATGGTTTCACTCGA	
AGAACTCGGTCTCCTGAAGATGGACTTCCTCGGACTCAAACCCCTCACAG	1800
AACTGAAACTCATGAAAGAACTCATAAAGGAAAGACACGGAGTGGATATA	
AACTTCCTTGAACTTCCCCCTTGACGACCCGAAAGTTTACAAACTCCTTCA	1900
GGAAGGAAAAACCACGGGAGTGTTCCAGCTCGAAAGCAGGGGAATGAAAG	
AACTCCTGAAGAACTAAAGCCCCGACAGCTTTGACGACATCGTTGCGGTC	2000
CTCGCACTCTACAGACCCCGACCTCTAAAGAGCGGACTCGTTGACACATA	
CATTAAGAGAAAGCACGGAAAAGAACCCGTTGAGTACCCCTTCCCGGAGC	2100
TTGAACCCGTCCTTAAGGAAACCTACGGAGTAATCGTTTATCAGGAACAG	
GTGATGAAGATGTCTCAGATACTTTCCGGCTTTACTCCCGGAGAGGGCGGA	2200
TACCTCAGAAAGGCGATAGGTAAGAAGAAAGCGGATTTAATGGCTCAGA	
TGAAAGACAAGTTTCATACAGGGAGCGGTGGAAAGGGGATACCCTGAAGAA	2300
AAGATAAGGAAGCTCTGGGAAGACATAGAGAAGTTTCGCTTCCTACTCCTT	
CAACAAGTCTCACTCGGTAGCTTACGGGTACATCTCCTACTGGACCGCCT	2400

FIG. 34A

ACGTTAAAGCCCACTATCCCGCGGAGTTCTTCGCGGTAAAACTCACAAC	
GAAAAGAACGACAACAAGTTCCTCAACCTCATAAAGACGCTAAACTCTT	2500
CGGATTTGAGATACTTCCCCCGACATAAACAAGAGTGATGTAGGATTTA	
CGATAGAAGGTGAAAACAGGATAAGGTTTCGGGCTTGCGAGGATAAAGGGA	2600
GTGGGAGAGGAACTGCTAAGATAATCGTTGAAGCTAGAAAGAAGTATAA	
GCAGTTCAAAGGGCTTGCGGACTTCATAAACAAAACCAAGAACAGGAAGA	2700
TAAACAAGAAAGTCGTGGAAGCACTCGTAAAGGCAGGGGCTTTTGACTTT	
ACTAAGAAAAAGAGGAAAGAACTACTCGCTAAAGTGGCAAACCTCTGAAAA	2800
AGCATTAATGGCTACACAAAACCTCCCTTTTCGGTGCACCGAAAGAAGAAG	
TGGAAGAACTCGACCCCTTAAAGCTTGAAAAGGAAGTTCTCGGTTTTTAC	2900
ATTTACAGGGCACCCCTTGACAACCTACGAAAAGCTCCTCAAGAACCGCTA	
CACACCCATTGAAGATTTAGAAGAGTGGGACAAGGAAAGCGAAGCGGTGC	3000
TTACAGGAGTTATCACGGAACCTCAAAGTAAAAAAGACGAAAAACGGAGAT	
TACATGGCGGTCTTCAACCTCGTTGACAAGACGGGACTAATAGAGTGTGT	3100
CGTCTTCCCGGGAGTTTACGAAGAGGCAAAGGAACCTGATAGAAGAGGACA	
GAGTAGTGGTAGTCAAAGGTTTTCTGGACGAGGACCTTGAAACGGAAAAT	3200
GTCAAGTTCGTGGTGAAAGAGGTTTTCTCCCCTGAGGAGTTCGCAAAGGA	
GATGAGGAATACCCTTTATATATTCTTAAAAAGAGAGCAAGCCCTAAACG	3300
GCGTTGCCGAAAAACTAAAGGGAATTATTGAAAACAACAGGACGGAGGAC	
GGATACAACCTTGGTTCTCACGGTTGATCTGGGAGACTACTTCGTTGATTT	3400
AGCACTCCCAAGATATGAACTAAAGGCTGACAGAAAGGTTGTAGAGG	
AGATAGAAAAACTGGGAGTGAAGGTCATAATTTAGTAAATAACCCTTACT	3500
TCCGAGTAGTCCCC	

FIG. 34B

MSKDFVHLHLHTQFSLLDGAIKIDELVKKAKEYGYKAVGMSDHGNLFGSY	
KFYKALKAEGIKPIIGMEAYFTTGSRFDRKTKTSEDNITDKYNHHLILIA	100
KDDKGLKNLMKLSTLAYKEGFYKPRIDYELLEKYGEGLIALTACLKGV	
TYYASINEVKKAEWVKFKDIFGDDLYLELQANNIPEQEVANRNLIIEIA	200
KKYDVKLIATQDAHYLNPEDRYAHTVLMALQMKKTIHELSSGNFKCSNED	
LHFAPPEYMWKKFEGKFEGWEKALLNTLEVMEKTADSFEIFENSTYLLPK	300
YDVPPDKTLEEYLRELAYKGLRQRIERGQAKDTKEYWERLEYELEVINKM	
GFAGYFLIVQDFINWAKKNDIPVGPGRGSAGGSLVAYAIGITDVPDIKHG	400
FLFERFLNPERVSMPPDIDVDFCQDNREKVIEWVRNKYGHDNVAQIITYNV	
MKAKQTLRDVARAMGLPYSTADKLAKLIPQGDVQGTWLSLEEMYKTPVEE	500
LLQKYGEHRTDIEDNVKKFRQICEESPEIKQLVETALKLEGLTRHTSLHA	
AGVVIAPKPLSELVPLYDKEGEVATQYDMVQLEELGLLKMDFLGLKTLT	600
ELKLMKELIKERHGVGINFLELPLDDPKVYKLLQEGKTTGVFQLESRGMK	
ELLKKLKPDSFDDIVAVLALYRPGPLKSGLVDTYIKRKHGKEPVEYPFPE	700
LEPVLKETYGIVIVYQEQVMKMSQILSGFTPGEADTLRKAIGKKKADLMAQ	
MKDKFIQGAVERGYPEEKIRKLWEDIEKFASYSFNKSHSVAYGYISYWTA	800
YVKAHYPAEFFAVKLTTEKNDNKFLNLIKDAKLFGFEILPPDINKSDVGF	
TIEGENRIRFGLARIKGVGEETAKIIVEARKKYKQFKGLADFINKTKNRK	900
INKKVVEALVKAGAFDFTKKRKELLAKVANSEKALMATQNSLFGAPKEE	
VEELDPLKLEKEVLGFYISGHPLDNYEKLLKNRYTPIEDLEEWKKESEAV	1000
LTGVITELKVKKTKNGDYMAVFNLDKTGLIECVVFPGVYEEAKELIEED	
RVVVVKGFLDEDLETENVKFVVKEVFSPEEFAKEMRNTLYIFLKREQALN	1100
GVAEKLKGIENNRTEDGYNLVLTVDLGDYFVDLALPQDMKLKADRKVVE	
EIEKLGVKVII	1161

FIG. 35

ATGAACTACGTTCCCTTCGCGAGAAAGTACAGACCGAAATTCTTCAGGGA	
AGTAATAGGACAGGAAGCTCCCGTAAGGATACTCAAAAACGCTATAAAAA	100
ACGACAGAGTGGCTCACGCCTACCTCTTTGCCGGACCGAGGGGGGTGGG	
AAGACGACTATTGCAAGAATTCTCGCAAAAGCTTTGAACTGTAAAAATCC	200
CTCCAAAGGTGAGCCCTGCGGTGAGTGCGAAAACTGCAGGGAGATAGACA	
GGGGTGTGTTCCCTGACTTAATTGAAATGGATGCCGCCTCAAACAGGGGT	300
ATAGACGACGTAAGGGCATTAAGAAGCGGTCAATTACAAACCTATAAA	
AGGAAAGTACAAGGTTTACATAATAGACGAAGCTCACATGCTCACGAAAG	400
AAGCTTTCAACGCTCTCTTAAAAACCTCGAAGAGCCCCCTCCCAGAACT	
GTTTTCGTCCTTTGTACCACGGAGTACGACAAAATTCTTCCACGATACT	500
CTCAAGGTGTCAGAGGATAATCTTCTCAAAGGTAAGAAAGGAAAAAGTAA	
TAGAGTATCTAAAAAGATATGTGAAAAGGAAGGGATTGAGTGCGAAGAG	600
GGAGCCCTTGAGGTTCTGGCTCATGCCTCTGAAGGGTGATGAGGGATGC	
AGCCTCTCTCCTGGACCAGGCGAGCGTTTACGGGGAAGGCAGGGTAACAA	700
AAGAAGTAGTGGAGAACTTCTCGGAATTCTCAGTCAGGAAAGCGTTAGG	
AGTTTTCTGAAATTGCTTCTGAACTCAGAAGTGGACGAAGCTATAAAGTT	800
CCTCAGAGAACTCTCAGAAAAGGGCTACAACCTGACCAAGTTTTGGGAGA	
TGTTAGAAGAGGAAGTGAGAAACGCAATTTTAGTAAAGAGCCTGAAAAAT	900
CCCGAAAGCGTGGTTCAGAACTGGCAGGATTACGAAGACTTCAAAGACTA	
CCCTCTGGAAGCCCTCCTCTACGTTGAGAACCTGATAAACAGGGGTAAAG	1000
TTGAAGCGAGAACGAGAGAACCCTTAAGAGCCTTTGAACTCGCGGTAATA	
AAGAGCCTTATAGTCAAAGACATAATTCCCGTATCCAGCTCGGAAGTGT	1100
GGTAAAGGAAACCAAAAAGGAAGAAAAGAAAGTTGAAGTAAAAGAAGAGC	
CAAAGTAAAAGAAGAAAAACCAAAGGAGCAGGAAGAGGACAGGTTCCAG	1200
AAAGTTTTAAACGCTGTGGACGGCAAAATCCTTAAAAGAATACTTGAAGG	
GGCAAAAAGGGAAGAAAGAGACGGAAAAATCGTCCTAAAGATAGAAGCCT	1300
CTTATCTGAGAACCATGAAAAAGGAATTTGACTCACTAAAGGAGACTTTT	
CCTTTTTTTAGAGTTTGAACCCGTGGAGGATAAAAAAAACCTCAGAAGTC	1400
CAGCGGGACGAGGCTGTTTTAAAGGTAAAGGAGCTCTTCAATGCAAAAAT	
ACTCAAAGTACGAAGTAAAAGCTAAGGTCATAAAGGTGAGAATGCCCGTG	1500
GAAGAGATAGGGCTGTTTAACGCACTAATAGACGGCTTGCCAGGTACGC	
ACTCACGAGGACGAAGGAAAAGGGAAAGGGAGAAGTTTTCGTTTTAGCGA	1600
CTCCTTATAAAGTCAAGGAATTGATGGAAGCTATGGAGGGTATGAAAAA	
CACATAAAGGATTTAGAAATCCTCGGAGAGACGGATGAGGATTTAACTTT	1700
TTAAAGTATGGGTGTATCTGAGCAAAGGTTTAAGCTAAAAACAAACCTGA	
AACCCGCAGGGGACCAGCCGAAAGCCATAAAAAAACTCCTTGAAAACCTA	1800
AGGAAAGGCGTAAAAGAACAAACACTTCTCGGAGTCACGGGAAGCGGAAA	
GACTTTTACTCTAGCAAACGTAATAGCGAAGTACAACAAACCAACTCTTG	1900
TGGTAGTTCACAACAAAATTCTCGCGGCACAGCTATACAGGGAGTTTAAA	
GAACTATTCCCTGAAAACGCTGTAGAGTACTTTGTCTCTTACTACGACTA	2000
TTACCAACCTGAAGCCTACATTCCTGAAAAAGATTTATACATAGAAAAGG	
ACGCGAGTATAAACGAAAGCTGGAACGTTTCAGACACTCCGCCACGATAT	2100
CCGTTCTAGAAAGGAGGGACGTTATAGTAGTTGCTTCAGTTTCTTGATA	
TACGGACTCGGGAAACCTGAGCACTACGAAAACCTGAGGATAAAACTCCA	2200
AAGGGGAATAAGACTGAACTTGAGTAAGCTCCTGAGGAAACTCGTTGAGC	
TAGGATATCAGAGAAATGACTTTGCCATAAAGAGGGCTACCTTCTCGGTT	2300
AGGGGAGACGTGGTTGAGATAGTCCCTTCTCACACGGAAGATTACCTCGT	
GAGGGTAGAGTTCTGGGACGACGAAGTTGAAAGAATAGTCCTCATGGACG	2400
CTCTGAAC	

FIG. 36

MNYVPFARKYRPKFFREVIGQEAPVRILKNAIKNDRVAHAYLFAGPRGVG	
KTTIARILAKALNCKNPSKGEPGECENCREIDRGVFPDLIEMDAASNRG	100
IDDVRLKEAVNYKPIKGKYKVYIIIDEAHMLTKEAFNALLKTLEPPPT	
VFVLCCTTEYDKILPTILSRCQRIIFSKVRKEKVIEYLKKICEKEGIECEE	200
GALEVLAHASEGCMRDAASLLDQASVYGEGRVTKEVVENFLGILSQESVR	
SFLKLLLNSEVDEAIKFLRELSEKGYNLTKFWEMLEEEVRNAILVKSLKN	300
PESVVQNWQDYEDFKDYPLEALLYVENLINRGKVEARTREPLRAFELAVI	
KSLIVKDIIPVSQLGSVVKETKKEEKKVEVKEEPKVKEEKPKEQEEDRFQ	400
KVLNAVDGKILKRILEGAKREERDGIIVLKIEASYLRTMKKEFDSLKETF	
PFLEFEPVEDKKKPQKSSGTRLF	473

FIG. 37

ATGCGCGTTAAGGTGGACAGGGAGGAGCTTGAAGAGGTTCTTAAAAAAGC	
AAGAGAAAGCACGGAAAAAAGCCGCACTCCCGATACTCGCGAACTTCT	100
TACTCTCCGCAAAAGAGGAAAACTTAATCGTAAGGGCAACGGACTTGGAA	
AACTACCTTGTAGTCTCCGTAAAGGGGGAGGTTGAAGAGGAAGGAGAGGT	200
TTGCGTCCACTCTCAAAAACCTCTACGATATAGTCAAGAACTTAAATTCCG	
CTTACGTTTACCTTCATACGGAAGGTGAAAAACTCGTCATAACGGGAGGA	300
AAGAGTACGTACAACTTCCGACAGCTCCCGCGGAGGACTTTCCCGAATT	
TCCAGAAATCGTAGAAGGAGGAGAAACACTTTTCGGGAAACCTTCTCGTTA	400
ACGGAATAGAAAAGGTAGAGTACGCCATAGCGAAGGAAGAAGCGAACATA	
GCCCTTCAGGGAATGTATCTGAGAGGATACGAGGACAGAATTCACCTTGT	500
GTTTCGGACGGTCACAGGCTTGCACTTTATGAACCTCTACGTAAACATTGA	
AAAGAGTGAAGACGAGTCTTTTGCTTACTTCTCCACTCCCGAGTGGAAC	600
TCGCCGTTAGCTCCTGGAAGGAGAATTCCCGGACTACATGAGTGTCATCC	
CTGAGGAGTTTTTCGGCGGAAGTCTTGTTTGAGACAGAGGAAGTCTTAAAG	700
GTTTTAAAGAGGTTGAAGGCTTTAAGCGAAGGAAAAGTTTTTCCCGTGAA	
GATTACCTTAAGCGAAAACCTTGCCATCTTTGAGTTCGCGGATCCGGAGT	800
TCGGAGAAGCGAGAGAGGAAATTGAAGTGGAGTACACGGGAGAGCCCTTT	
GAGATAGGATTCAACGGAAATACCTTATGGAGGCGCTTGACGCCTACGAC	900
AGCGAAAGAGTGTGGTTCAAGTTCACAACCCCGACACGGCCACTTTATT	
GGAGGCTGAAGATTACGAAAAGGAACCTTACAAGTGCATAATAATGCCGA	1000
TGAGGGTGTAGCCATGAAAAAGCTTTAATCTTTTTATTGAGCTTGAGCC	
TTTTAATTCCTGCGTTTAGCGAAGCCAAACCCAAGTCTTC	1090

FIG. 38

MRVKVDREELEEVLKKARESTEKKAALPILANFLLSAKEENLIVRATDLE	
NYLVSVKGEVEEEGEVVCVHSQKLYDIVKNLNSAYVYLHTEGEKLVITGG	100
KSTYKLPTAPAEDFPEFPEIVEGGETLSGNLLVNGIEKVEYAIKEEANI	
ALQGYLRGYEDRIHFVGS DGHRLALYEPLGEFSKELLI PRKSLKVLKKL	200
ITGIEDVNIKSEDES FAYFSTPEWKLA VRLLEGEFPDYMSVIPEEFSAE	
VLFETEEVLKVLKRLKALSEGKVFPVKITLSENLAIFEADPEFGEAREE	300
IEVEYTGEPFEIGFNGKYLMEALDAYDSERVWFKFTTPDTATLLEAEDYE	
KEPYKCIIMPMRV	363

FIG. 39

GTGGAAACCACAATATTCCAGTTCCAGAAAACCTTTTTTCACAAAACCTCC	
GAAGGAGAGGGTCTTCGTCTTCATGGAGAAGAGCAGTATCTCATAAGAA	100
CCTTTTTGTCTAAGCTGAAGGAAAAGTACGGGGAGAATTACACGGTTCTG	
TGGGGGGATGAGATAAGCGAGGAGGAATTCTACACTGCCCTTTCCGAGAC	200
CAGTATATTTCGGCGGTTCAAAGGAAAAAGCGGTGGTCATTTACAACCTTCG	
GGGATTTCTGAAGAAGCTCGGAAGGAAGAAAAAGGAAAAAGAAAGGCTT	300
ATAAAAGTCCTCAGAAACGTAAAGAGTAACTACGTATTTATAGTGATACGA	
TGCGAAACTCCAGAAACAGGAACTTTCTTCGGAACCTCTGAAATCCGTAG	400
CGTCTTTTCGGCGGTATAGTGGTAGCAAACAGGCTGAGCAAGGAGAGGATA	
AAACAGCTCGTCCTTAAGAAGTTCAAAGAAAAAGGGATAAACGTAGAAAA	500
CGATGCCCTTGAATACCTTCTCCAGCTCACGGGTACAACTTGATGGAGC	
TCAAACCTTGAGGTTGAAAAACTGATAGATTACGCAAGTGAAAAGAAAATT	600
TTAACACTCGATGAGGTAAAGAGAGTAGCCTTCTCAGTCTCAGAAAACGT	
AAACGTATTTGAGTTCGTTGATTTACTCCTCTTAAAAGATTACGAAAAGG	700
CTCTTAAAGTTTTGGACTCCCTCATTTCTTCGGAATACACCCCTCCAG	
ATTATGAAAATCCTGTCCTCCTATGCTCTAAAACCTTACACCCTCAAGAG	800
GCTTGAAGAGAAGGGAGAGGACCTGAATAAGGCGATGGAAAGCGTGGGAA	
TAAAGAACAACCTTTCTCAAGATGAAGTTCAAATCTTACTTAAAGGCAAAC	900
TCTAAAGAGGACTTGAAGAACCTAATCCTCTCCCTCCAGAGGATAGACGC	
TTTTTCTAACTTTACTTTTCAAGACACAGTGCAGTTGCTGGGGATTTCTT	1000
GACCTCAAGACTGGAGAGGGAAGTTGTGAAAAATACTTCTCATGGTGGAT	
AATCTTTTTTATGAAGTTTGCAGTTTTCGTTTTTCCCGGTTCT	1093

FIG. 40

VETTIFQFQKTFFTKPPKERVFLHGEEQYLIRTFLLSKLKEKYGENYTVL	
WGDEISEEEFYTALSETSIFFGSKEKAVVIYNFGDFLKKLGRKKKEKERL	100
IKVLRNVKSNYVFIVYDAKLQKQELSSEPLKSVASFGGIVVANRLSKERI	
KQLVLKKFKEKGINVENDALEYLLQLTGYNLMELKLEVEKLIDYASEKKI	200
LTLDEVKRVAFSVSENVNVFEFVDLLLLLDYKALKVLDLSLISFGIHPLO	
IMKILSSYALKLYTLKRLEEKGEDLNKAMESVGIKNNFLKMKFKSYLKAN	300
SKEDLKNLILSLQRIDAFSKLYFQDTVQLLRDFLTSLRLEREVVKNTSHGG	

FIG. 41

ATGGAAAAAGTTTTTTTGGAAAACTCCAGAAAACCTTGCCACATACCCGG	
AGGACTCCTTTTTTACGGCAAAGAAGGAAGCGGAAAGACGAAAAACAGCTT	100
TTGAATTTGCAAAGGTATTTTATGTAAGGAAAACGTACCTGGGGATGCG	
GAAGTTGTCCCTCCTGCAAACACGTAAACGAGCTGGAGGAAGCCTTCTTT	200
AAAGGAGAAATAGAAGACTTTAAAGTTTATAAGACAAGGACGGTAAAAAG	
CACTTCGTTTACCTTATGGGCGAACATCCCGACTTTGTGGTAATAATCCC	300
GAGCGGACATTACATAAAGATAGAACAGATAAGGGAAGTTAAGAACTTTG	
CCTATGTGAAGCCCGCACTAAGCAGGAGAAAAGTAATTATAATAGACGAC	400
GCCACGCGATGACCTCTCAGGCGGCAAACGCTCTTTTAAAGGTATTGGA	
AGAGCCACCTGCGGACACCACCTTTATCTTGACCACGAACAGGCGTTCTG	500
CAATCCTGCCGACTATCCTCTCCAGAACTTTTCAAGTGGAGTTCAAGGGC	
TTTTTCAGTAAAAGAGGTTATGGAAATAGCGAAAGTAGACGAGGAAATAGC	600
GAAACTCTCTGGAGGCAGTCTAAAAGGGCTATCTTACTAAAGGAAAACA	
AAGATATCCTAAACAAAGTAAAGGAATTCTTGGAACCGAGCCGTTAAAA	700
GTTTACAAGCTTGCAAGTGAATTCGAAAAGTGGGAACCTGAAAAGCAAAA	
ACTCTTCCTTGAAATTATGGAAGAATTGGTATCTCAAAAATTGACCGAAG	800
AGAAAAAAGACAATTACACCTACCTTCTTGATACGATCAGACTCTTTAAA	
GACGGACTCGCAAGGGGTGTAAACGAACCTCTGTGGCTGTTTACGTTAGC	900
CGTTCAGGCGGATTAAATAAACCGTTATTGATTCCGTAACATTTAAACCTT	
AATCTAAATTATGAGAGCCTTTGAAGGAGGTCTGGTATGGAAAATTTGAA	1000
GATTAGATATATAGATACGAGGAAGATAGGAACCGTGAGCGGTGTAAAAG	
T	1051

FIG. 42

MEKVFLEKLQKTLHIPGGLLFYKGESGKTKTAFEFAKGILCKENVPWGC	
GSCPSCKHVNELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVI	100
PSGHYIKIEQIREVKNFAYVKPALSRKVI IIDDAHAMTSQAANALLKVL	
EEPPADTTFILTTNRRSAILPTILSRTFQVEFKGFSVKEVMEIAKVDEEI	200
AKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLASEFEKWEPEKQ	
KLFLIMEELVSQKLTEKKDNYTYLLDTIRLFKDGGLARGVNEPLWLFTL	300
AVQAD	

FIG. 43

ATGAACTTCCTGAAAAAGTTCCTTTTACTGAGAAAAGCTCAAAAGTCTCC
 TTACTIONTTCGAAGAGTTCTACGAAGAAATCGATTTGAACCAGAAGGTGAAAG 100
 ATGCAAGGTTTGTAGTTTTTACTGCGAAGCCACAGAACTCGACGTAAAG
 AAGGCAAACTCCTTTCAATAGGTGCGGTTGAGGTTAAAAACCTGGAAAT 200
 AGACCTCTCTAAATCTTTTACGAGATACTCAAAAGTGACGAGATAAAGG
 CGGCGGAGATACATGGAATAACCAGGGAAGACGTTGAAAAGTACGGAAAG 300
 GAACCAAAGGAAGTAATATACGACTTCTGAAGTACATAAAGGGAAGCGT
 TCTCGTTGGCTACTACGTGAAGTTTGACGTCTCACTCGTTGAGAAGTACT 400
 CCATAAAGTACTTCCAGTATCCAATCATCAACTACAAGTTAGACCTGTTT
 AGTTTCGTGAAGAGAGAGTACCAGAGTGGCAGGAGTCTTGACGACCTTAT 500
 GAAGGAACTCGGTGTAGAAATAAGGGCAAGGCACAACGCCCTTGAAGATG
 CCTACATAACCGCTCTTCTTTTCTAAAGTACGTTTACCCGAACAGGGAG 600
 TACAGACTAAAGGATCTCCCGATTTTCCTT

FIG. 44

MNFLKKFLLLKKAQKSPYFEEFYEEIDLNQKVKDARFVVFDCEATELDVK
 KAKLLSIGAVEVKNLEIDLKSFYEILKSDEIKAAEIHGITREDVEKYGK 100
 EPKEVIYDFLKYIKGSVLVGYYVKFDVSLVEKYSIKYFQYPIINYKLDLF
 SFVKREYQSGRSLDDLMKELGVEIRARHNALEDAYITALLFLKYVYPNRE 200
 YRLKDLPIFL

FIG. 45

ATGCTCAATAAGGTTTTTATAATAGGAAGACTTACGGGTGACCCCGTTAT	
AACTTATCTACCGAGCGGAACGCCCCTAGTAGAGTTTACTCTGGCTTACA	100
ACAGAAGGTATAAAAACCAGAACGGTGAATTTTCAGGAGGAAAGTCACTTC	
TTTGACGTAAAGGCGTACGGAAAAATGGCTGAAGACTGGGCTACACGCTT	200
CTCGAAAGGATACCTCGTACTCGTAGAGGGAAGACTCTCCAGGAAAAGT	
GGGAGAAAGAAGGAAAGAAGTTCTCAAAGGTCAGGATAATAGCGGAAAAC	300
GTAAGATTAATAAACAGGCCGAAAGGTGCTGAACTTCAAGCAGAAGAAGA	
GGAGGAAGTTCCTCCCATTGAGGAGGAAATTGAAAACTCGGTAAAGAGG	400
AAGAGAAGCCTTTTACCGATGAAGAGGACGAAATACCTTTTTTAATTTGA	
GGAGGTTAAAGTATGGTAGTGAGAGCTCCTAAGAAGAAAGTTTGTATGTA	500
CTGTGAACAAAAGAGAGAGCCAGATT	

FIG. 46

MLNKVFIIGRLTGDPVITYLPSGTPVVEFTLAYNRRYKNQNGEFQEE SHF	
FDVKAYGKMAEDWATRFSGYLVLEGRLSQEKWEKEGKKFSKVRIIAEN	100
VRLINRPKGAE LQAEEEEVPPIEEEIEKLGKEEEKPFTDEEDEI PF	

FIG. 47

ATGCAATTTGTGGATAAACTTCCCTGTGACGAATCCGCCGAGAGGGCGGT	
TCTTGGCAGTATGCTTGAAGACCCCGAAAACATACCTCTGGTACTTGAAT	100
ACCTTAAAGAAGAAGACTTCTGCATAGACGAGCACAAGCTACTTTTCAGG	
GTTCTTACAAACCTCTGGTCCGAGTACGGCAATAAGCTCGATTTCGTATT	200
AATAAAGGATCACCTTGAAAAGAAAACTTACTCCAGAAAATACCTATAG	
ACTGGCTCGAAGAACTCTACGAGGAGGCGGTATCCCCTGACACGCTTGAG	300
GAAGTCTGCAAAATAGTAAAACAACGTTCCGCACAGAGGGCGATAATTCA	
ACTCGGTATAGAACTCATTACAAAGGAAAGGAAAACAAAGACTTTTCA	400
CATTAATCGAGGAAGCCAGAGCAGGATATTTTCCATAGCGGAAAGTGCT	
ACATCTACGCAGTTTTTACCATGTGAAAGACGTTGCGGAAGAAGTTATAGA	500
ACTCATTTATAAATTCAAAGCTCTGACAGGCTAGTCACGGGACTCCCAA	
GCGGTTTCACGGAACCTCGATCTAAAGACGACGGGATTCCACCCTGGAGAC	600
TTAATAATACTCGCCGAAGACCCGGTATGGGGAAAACCGCCTTTATGCT	
CTCCATAATCTACAATCTCGCAAAAGACGAGGGAAAACCTCAGCTGTAT	700
TTTCCTTGGAAATGAGCAAGGAACAGCTCGTTATGAGACTCCTCTCTATG	
ATGTCGGAGGTCCCACCTTTTCAAGATAAGGTCTGGAAGTATATCGAATGA	800
AGATTTAAAGAAGCTTGAAGCAAGCGCAATAGAACTCGCAAAGTACGACA	
TATACCTCGACGACACACCCGCTCTCACTACAACGGATTTAAGGATAAGG	900
GCAAGAAAGCTCAGAAAGGAAAAGGAAGTTGAGTTCGTGGCGGTGGACTA	
CTTGCAACTTCTGAGACCGCCAGTCCGAAAGAGTTCAAGACAGGAGGAAG	1000
TGGCAGAGGTTTCAAGAACTTAAAAGCCCTTGCAAAGGAACTTCACATT	
CCCGTTATGGCACTTGCGCAGCTCTCCCGTGAGGTGGAAAAGAGGAGTGA	1100
TAAAAGACCCAGCTTGCGGACCTCAGAGAATCCGGACAGATAGAACAGG	
ACGCAGACCTAATCCTTTTCTCCACAGACCCGAGTACTACAAGAAAAAG	1200
CCAAATCCCGAAGAGCAGGGTATAGCGGAAGTGATAATAGCCAAGCAAAG	
GCAAGGACCCACGGACATTGTGAAGCTCGCATTTATTAAGGAGTACACTA	1300
AGTTTGCAAACCTAGAAGCCCTTCTGAACAACCTCCTGAAGAAGAGGAA	
CTTTCCGAAATTATTGAAACACAGGAGGATGAAGGATTGAAGATATTGA	1400
CTTCTGAAAATTAAGGTTTTATAATTTTATCTTGGCTATCCGGGGTAGCT	
CAATCGGCAGAGCGGGTGGCTG	1472

FIG. 48

MQFVDKLPCEDESAERAVLGSMLEDPENIPLVLEYLKEEDFCIDEHKLLFR	
VLTNLWSEYGNKLDVFLIKDHLEKKNLLQKIPIDWLEELYEEAVSPDTLE	100
EVCKIVKQRSAQRAIIQLGITSTQFYHVKDVAEEVIELIYKFKSSDRLVT	
GLPSGFTELDLKTTFHFGDLII LAARPGMGKTAFLMSIIYNLAKDEGKP	200
SAVFSLEMSKEQLVMRLLSMMSEVPLFKIRSGSISNEDLKKLEASAIELA	
KYDIYLDTPALTTTDLRIRARKLRKEKEVEFVAVDYQLQLLRPPVRKSSR	300
QEEVAEVSRLKALAKELHIPVMALAQLSREVEKRSDKRPQLADLRESGQ	
IEQDADLILFLHRPEYYKKKPNPEEQGIAEVIIAKQRQGPTDIVKLAFIK	400
EYTKFANLEALPEQPPEEEELSEIIETQDEDEGFEDIDF	

FIG. 49

ATGTCCTCGGACATAGACGAACTTAGACGGGAAATAGATATAGTAGACGT	
CATTTCCGAATACTTAACTTAGAGAAGGTAGGTTCCAATTACAGAACGA	100
ACTGTCCCTTTACCCTGACGATACACCCTCCTTTTACGTGTCTCCAAGT	
AAACAAATATTCAAGTGTTTCGGTTGCGGGGTAGGGGAGACGCGATAAA	200
GTTTCGTTTTCCCTTTACGAGGACATCTCCTATTTTGAAGCCGCCCTTGAAC	
TCGCAAAACGCTACGGAAGAAATTAGACCTTGAAAAGATATCAAAAGAC	300
GAAAAGGTATACGTGGCTCTTGACAGGGTTTGTGATTCTACAGGGAAAG	
CCTTCTCAAAAACAGAGAGGCAAGTGAGTACGTAAAGAGTAGGGGAATAG	400
ACCCTAAAGTAGCGAGGAAGTTTGATCTTGGGTACGCACCTTCCAGTGAA	
GCACTCGTAAAGTCTTAAAAGAGAACGATCTTTTAGAGGCTTACCTTGA	500
AACTAAAAACCTCCTTTCTCCTACGAAGGGTGTTTACAGGGATCTCTTTC	
TTCCGGCGTGTCGTGATCCCGATAAAGGATCCGAGGGGAAGAGTTATAGGT	600
TTCCGGTGGAAGGAGGATAGTAGAGGACAAATCTCCCAAGTACATAAACTC	
TCCAGACAGCAGGGTATTTAAAAGGGGGAGAACTTATTCGGTCTTTACG	700
AGGCAAAGGAGTATATAAAGGAAGAAGGATTTGCGATACTTGTGGAAGGG	
TACTTTGACCTTTTGAGACTTTTTTCCGAGGGAATAAGGAACGTTGTTGC	800
ACCCCTCGGTACAGCCCTGACCCAAAATCAGGCAAACCTCCTTTCCAAGT	
TCACAAAAAAGGTCTACATCCTTTACGACGGAGATGATGCGGGAAGAAAG	900
GCTATGAAAAGTGCCATTTCCCTACTCCTCAGTGCAGGAGTGGAAGTTTA	
TCCCGTTTACCTCCCCGAAGGATACGATCCCGACGAGTTTATAAAGGAAT	1000
TCGGGAAAGAGGAATTAAGAAGACTGATAAACAGCTCAGGGGAGCTCTTT	
GAAACGCTCATAAAAACCGCAAGGGAAAACCTTAGAGGAGAAAACGCGTGA	1100
GTTTCAGGTATTATCTGGGCTTTATTTCCGATGGAGTAAGGCGCTTTGCTC	
TGGCTTCGGAGTTTACACCAAGTACAAAGTTTCTATGGAAATTTTATTA	1200
ATGAAAATTGAAAAAAATTCTCAAGAAAAAGAAATTAACTCTCCTTTAA	
GGAAAAAATCTTCCTGAAAGGACTGATAGAATTAAACCAAAAATAGACC	1300
TTGAAGTCCTGAACTTAAGTCCTGAGTTAAAGGAACTCGCAGTTAACGCC	
TTAAACGGAGAGGAGCATTTACTTCCAAAAGAAGTTCTCGAGTACCAGGT	1400
GGATAACTTGGAGAACTTTTAAACAACATCCTTAGGGATTTACAAAAAT	
CTGGGAAAAAGAGGAAGAAAAGAGGGTTGAAAAATGTAAATACTTAATTA	1500
ACTTTAATAAATTTTATAGAGTTAGGA	

FIG. 50

MSSDIDELRREIDIVDVISEYLNLEKVGSNYRTNCPFHPDDTPSFYVSPS	
KQIFKCFGCGVGDAIKFVSLYEDISYFEAALELAKRYGKKLDLEKISKD	100
EKVYVALDRVCDFYRESLLKNREASEYVKSRGIDPKVARKFDLGYAPSSE	
ALVKVLKENDLLEAYLETKNLLSPTKGVYRDLFLRRVVIPIKDPRGRVIG	200
FGRRIVEDKSPKYINSPDSRVFKKGENLFGLYEAKYIKEEGFAILVEG	
YFDLLRLFSEGIRNVVAPLGTALTQNQANLLSKFTKKVYILYDGDDAGRK	300
AMKSAIPLLLSAGVEVYPVYLPEGYDPDEFIKEFGKEELRRLINSSGELF	
ETLIKARENLEEKTRFRYYLGFISDGVRRFALASEFHTKYKVPMEILL	400
MKIEKNSQEKEIKLSFKEKIFLKGLIELKPKIDLEVLNLSPELKELAVNA	
LNGEEHLLPKEVLEYQVDNLEKLFNNILRDLQKSGKKRKRGLKNVNT	498

FIG. 51

ATGCAAGATACCGCTACCTGCAGTATTTGTCAGGGGACGGGATTTCGTAAA	
GACCGAAGACAACAAGGTAAGGCTCTGCGAATGCAGGTTCAAGAAAAGGG	100
ATGTAAACAGGGAACTAAACATCCCAAAGAGGTACTGGAACGCCAACTTA	
GACACTTACCACCCCAAGAACGTATCCCAAGAACAGGGCACTTTTGACGAT	200
AAGGGTCTTCGTCCACAACCTTCAATCCCGAGGAAGGGAAAGGGCTTACCT	
TTGTAGGATCTCCTGGAGTCGGCAAACTCACCTTGCGGTTGCAACATTA	300
AAAGCGATTTATGAGAAGAAGGGAATCAGAGGATACTTCTTCGATACGAA	
GGATCTAATATTCAGGTAAAAACACTTAATGGACGAGGGAAAGGATACAA	400
AGTTTTTAAAAACTGTCTTAAACTCACCGGTTTTGGTTCTCGACGACCTC	
GGTTCTGAGAGGCTCAGTGACTGGCAGAGGGAACCTCATCTCTTACATAAT	500
CACCTACAGGTATAACAACCTTAAGAGCACGATAATAACCACGAATTACT	
CACTCCAGAGGGAAGAAGAGAGTAGCGTGAGGATAAGTGCGGATCTTGCA	600
AGCAGACTCGGAGAAAACGTAGTTTCAAAAATTTACGAGATGAACGAGTT	
GCTCGTTATAAAGGGTTCCGACCTCAGGAAGTCTAAAAAGCTATCAACCC	700
CATCT	

FIG. 52

MQDTATCSICQGTGFVKTEDNKNVRLCECRFKKRDVNRELNIPKRYWNANL	
DTYHPKNVSNRALLTIRVFVHNFNP EEGKGLTFVGSPGVGKTHLAVATL	100
KAIYEKKGIRGYFFDTKD LIFRLKHLMD EGKDTKFLKTVLNSPVLVDDL	
GSERLSDWQRELISYIITYRYNNLKSTIITTNYSLQREEESSVRISADLA	200
SRLGENVVSKIYEMNELLVIKGS DLRKSKKLSTPS	

FIG. 53

ATGAAAAAGATTGAAAATTTGAAGTGGAAAAATGTCTCGTTTAAAAGCCT	100
GGAAATAGATCCCGATGCAGGTGTGGTTCTCGTTTCCGTGGAAAAATTCT	
CCGAAGAGATAGAAGACCTTGTGCGTTTACTGGAGAAGAAGACGCGGTTT	200
CGAGTCATCGTGAACGGTGTTCAAAAAAGTAACGGGGATCTAAGGGGAAA	
GATACTTTCCCTTCTCAACGGTAATGTGCCTTACATAAAAGATGTTGTTT	300
TCGAAGGAAACAGGCTGATTCTGAAAGTGCTTGGAGATTTGCGCGGGGAC	
AGGATCGCCTCCAACTCAGAAGCACGAAAAAACAGCTCGATGAACTGCT	400
GCCTCCCGGAACAGAGATCATGCTGGAGGTTGTGGAGCCTCCGGAAGATC	
TTTTGAAAAAGGAAGTACCACAACCAGAAAAGAGAGAAGAACCAAAGGGT	500
GAAGAATTGAAGATCGAGGATGAAAACCACATCTTTGGACAGAAACCCAG	
AAAGATCGTCTTCACCCCCCTCAAAAATCTTTGAGTACAACAAAAAGACAT	600
CGGTGAAGGGCAAGATCTTCAAAATAGAGAAGATCGAGGGGAAAAGAACG	
GTCCTTCTGATTTACCTGACAGACGGAGAAGATTCTCTGATCTGCAAAGT	700
CTTCAACGACGTTGAAAAGGTCGAAGGGGAAAGTATCGGTGGGAGACGTGA	
TCGTTGCCACAGGAGACCTCCTTCTCGAAAACGGGGAGCCCACCCTTTAC	800
GTGAAGGGAATCACAAAACCTCCCGAAGCGAAAAGGATGGACAAATCTCC	
GGTTAAGAGGGTGGAGCTCCACGCCCATAACCAAGTTCAGCGATCAGGACG	900
CAATAACAGATGTGAACGAATATGTGAAACGAGCCAAGGAATGGGGCTTT	
CCCGCGATAGCCCTCACGGATCATGGGAACGTTCAGGCCATACCTTACTT	1000
CTACGACGCGGCGAAAGAAGCTGGAATAAAGCCCATTTTCGGTATCGAAG	
CGTATCTGGTGAGTGACGTGGAGCCCGTCATAAGGAATCTCTCCGACGAT	1100
TCGACGTTTGGAGATGCCACGTTCTGTCGTCTCGACTTCGAGACGACGGG	
TCTCGACCCGCAGGTGGATGAGATCATCGAGATAGGAGCGGTGAAGATAC	1200
AGGGTGGCCAGATAGTGGACGAGTACCACACTCTCATAAAGCCTTCCAGG	
GAGATCTCAAGAAAAAGTTCGGAGATCACCGGAATCACTCAAGAGATGCT	1300
GGAAAACAAGAGAAGCATCGAGGAAGTTCGCGGAGTTCTCGGTTTTC	
TGGAAGATTCCATCATCGTAGCACACAACGCCAACTTCGACTACAGATTT	1400
CTGAGGCTGTGGATCAAAAAAGTGATGGGATTGGACTGGGAAAGACCCTA	
CATAGATACGCTCGCCCTCGCAAAGTCCCTTCTCAAAGTGAAGCTACT	1500
CTCTGGATTCCGTTGTGGAAGAGCTCGGATTGGGTCCCTTCCGGCACCAC	
AGGGCCCTGGATGACGCGAGGGTCAACGCTCAGGTTTTCTCAGGTTTCGT	1600
TGAGATGATGAAGAAGATCGGTATCACGAAGCTTTCAGAAATGGAGAAGT	
TGAAGGATACGATAGACTACACCGCGTTGAAACCCTTCCACTGCACGATC	1700
CTCGTTCAGAACAAAAAGGGATTGAAAAACCTATACAACTGGTTTCTGA	
TTCTATATAAAGTACTTCTACGGTGTTCCGAGGATCCTCAAAGTGAGC	1800
TCATCGAGAACAGAGAAGGACTGCTCGTGGGTAGCGCGTGATCTCCGGT	
GAGCTCGGACGTGCCGCCCTCGAAGGAGCGAGTGATTGAGAACTCGAAGA	1900
GATCGCGAAGTTCTACGACTACATAGAAGTCATGCCGCTCGACGTTATAG	
CCGAAGATGAAGAAGACCTAGACAGAGAAAGACTGAAAGAAGTGTAACGA	2000
AAACTCTACAGAATAGCGAAAAAATTGAACAAGTTCGTGTCATGACCGG	
TGATGTTTCAATTTCTCGATCCCGAAGATGCCAGGGGCAGAGCTGCACTTC	2100
TGGCACCTCAGGGAAACAGAACTTCGAGAATCAGCCCGCACTCTACCTC	
AGAACGACCGAAGAAATGCTCGAGAAGGCGATAGAGATATTCGAAGATGA	2200
AGAGATCGCGAGGGAAAGTCGTGATAGAGAATCCCAACAGAATAGCCGATA	
TGATCGAGGAAGTGCAGCCGCTCGAGAAAAAACTTCACCCGCCGATCATA	2300
GAGAACGCCGATGAAATAGTGAGAAACCTCACCATGAAGCGGGCGTACGA	
GATCTACGGTGATCCGCTTCCCGAAATCGTCCAGAAGCGTGTGAAAAAGG	

FIG. 54A

AACTGAACGCCATCATAAATCATGGATACGCCGTTCTCTATCTCATCGCT	2400
CAGGAGCTCGTTCAGAAATCTATGAGCGATGGTTACGTGGTTGGATCCAG	
AGGATCCGTCGGGTCTTCACTCGTGGCCAATCTCCTCGGAATAACAGAGG	2500
TGAATCCCCTACCACCACATTACAGGTGTCCAGAGTGCAAATACTTTGAA	
GTTGTCTGAAGACGACAGATACGGAGCGGGTTACGACCTTCCCAACAAGAA	2600
CTGTCCAAGATGTGGGGCTCCTCTCAGAAAAGACGGCCACGGCATAACCGT	
TTGAAACGTTTCATGGGGTTCGAGGGTGACAAGGTCCCCGACATAGATCTC	2700
AACTTCTCAGGAGAGTATCAGGAACGTGCTCATCGTTTTGTGGAAGAACT	
CTTCGGTAAAGACCACGTCTATAGGGCGGGAACCATAAACACCATCGCGG	2800
AAAGAAGTGCGGTGGGTACGTGAGAAGCTACGAAGAGAAAACCGGAAAG	
AAGCTCAGAAAGGCGGAAATGGAAAGACTCGTTTCCATGATCACGGGAGT	2900
GAAGAGAACGACGGGTGAGCACCAGGGGGGCTCATGATCATAACCGAAAG	
ACAAAGAAGTCTACGATTTCACTCCCATACAGTATCCAGCCAACGATAGA	3000
AACGCAGGTGTGTTCAACACGCACTTCGCATACGAGACGATCCATGATGA	
CCTGGTGAAGATAGATGCGCTCGGCCACGATGATCCCACTTTCATCAAGA	3100
TGCTCAAGGACCTCACCGGAATCGATCCCATGACGATTCCCATGGATGAC	
CCCGATACGCTCGCCATATTCAGTTCTGTGAAGCCTCTTGGTGTGGATCC	3200
CGTTGAGCTGGAAAGCGATGTGGGAACGTACGGAATTCCGGAGTTCGGAA	
CCGAGTTTGTGAGGGGAATGCTCGTTGAAACGAGACCAAAGAGTTTCGCC	3300
GAGCTTGTGAGAATCTCAGGACTGTACACGGTACGGACGTCTGGTTGAA	
CAACGCACGTGATTGGATAAACCTCGGCTACGCCAAGCTCTCCGAGGTTA	3400
TCTCGTGTAGGGACGACATCATGAACTTCCTCATACACAAAGGAATGGAA	
CCGTCACCTTGCCTTCAAGATCATGGAAAACGTCAGGAAGGGAAAGGGTAT	3500
CACAGAAGAGATGGAGAGCGAGATGAGAAGGCTGAAGGTTCCAGAATGGT	
TCATCGAATCCTGTAAAAGGATCAAATATCTCTTCCCGAAAGCTCACGCT	3600
GTGGCTTACGTGAGTATGGCCTTCAGAATTGCTTACTTCAAGGTTCACTA	
TCCTCTTCAGTTTTACGCGGCGTACTTCACGATAAAAGGTGATCAGTTTCG	3700
ATCCGGTTCTCGTACTCAGGGGAAAAGAAGCCATAAAGAGGCGCTTGAGA	
GAACTCAAAGCGATGCCTGCCAAAGACGCCCAGAAGAAAAACGAAGTGAG	3800
TGTTCTGGAGGTTGCCCTGGAAATGATACTGAGAGGTTTTTCTTCTCTAC	
CGCCCGACATCTTCAAATCCGACGCGAAGAAATTTCTGATAGAAGGAAAC	3900
TCGCTGAGAATTCGGTTCAACAACTTCCAGGACTGGGTGACAGCGTTGC	
CGAGTCGATAATCAGAGCCAGGGAAGAAAAGCCGTTCACTTCGGTGGAAG	4000
ATCTCATGAAGAGGACCAAGGTCAACAAAAATCACATAGAGCTGATGAAA	
AGCCTGGGTGTTCTCGGGGACCTTCCAGAGACGGAACAGTTCACGCTTTT	4100

C

FIG. 54B

MKKIENLKWKNVSFKSLEIDPDAGVVLVSVEKFSEEIEDLVRLLEKKTRF	
RVIVNGVQKSNGDLRGKILSLLNGNVPYIKDVVFEGNRLILKVLGDFARD	100
RIASKLRSTKKQLDELLPPGTEIMLEVVEPPEDLLKKEVPQPEKREEPKG	
EELKIEDENHIFGQKPRKIVFTPSKIFEYNKTSVKGKIFKIEKIEGKRT	200
VLLIYLTGDGDSLICKVFNDVEKVEGKVSVDVIVATGDLLLENGEPTLY	
VKGITKLPEAKRMDKSPVKRVELHAHTKFSQDAITDVNEYVKRAKEWGF	300
PAIALTDHGNVQAIPYFYDAAKEAGIKPIFGIEAYLVSDVEPVIRNLSDD	
STFGDATFVVLDFETTGLDPQVDEIIIEIGAVKIQGGQIVDEYHTLIKPSR	400
EISRKSSSEITGITQEMLENKRSIEEVLPEFLGFLIEDSIIIVAHNANFDYRF	
LRLWIKKVMGLDWERPYIDTLALAKSLLKLSYSLDSVVEKLGLGPFRHH	500
RALDDARVTAQVFLRFVEMMKIGITKLSEMEKLKDTIDYTALKPFHCTI	
LVQNKKGKLNLYKLVSDSYIKYFYGVPRILKSELINREGLLVGSACISG	600
ELGRAALEGASDSELEEIAKFYDYIEVMPLDVIAEDEEDLDRERLKEVYR	
KLYRIAKKLNKFVVMTGDVHFLDPEDARGRAALLAPQGNRNFFENQPALYL	700
RTTEEMLEKAIEIFEDEEIIAREVVIENPNRIADMIEEVQPLEKKLHPPII	
ENADEIVRNLTMKRAYEIIYGDPLPEIVQKRVEKELNAIINHGYAVLYLIA	800
QELVQKSMSDGYVVGSRGSSVLNLLGITEVNPLPPHYRCPECKYFE	
VVEDDRYGAGYDLPNKNCPRCGAPLRKDGHGIPFETFMGFEGDKVPDIDL	900
NFSGEYQERAHRFVEELFGKDHVYRAGTINTIAERSAVGYVRSYEETGK	
KLRKAEMERLVSMITGVKRTTGQHPGGLMIIPKDKEVYDFTPIQYPANDR	1000
NAGVFTTHFAYETIHDDLVKIDALGHDDPTFIKMLKDLTGIDPMTIPMDD	
PDTLAIFSSVKPLGVDPVELESVDGTYGIPEFGTEFVRGMLVETRPKSFA	1100
ELVRISGLSHGTDVWLNWARDWINLGYAKLSEVISCRDDIMNFLIHGME	
PSLAFKIMENVRKGGKITEEMESEMRRLKVPEWFIESCKRIKYLFPKAHA	1200
VAYVSMAFRIAYFKVHYPLQFYAAYFTIKGDQFDPVLVLRGKEAIKRRRL	
ELKAMPAKDAQKNEVSVLEVALEMILRGFSFLPPDIFKSDAKKFLIEGN	1300
SLRIPFNKLPLGLGDSVAESIIRAREEKPFSTSVEDLMKRTKVNKNHIELMK	
SLGVLGDLPETEQFTLF	1367

FIG. 55

GTGCTCGCCATGATATGGAACGACACCGTTTTTTGCGTCGTAGACACAGA	
AACCACGGGAACCGATCCCTTTGCCGGAGACCGGATAGTTGAAATAGCCG	100
CTGTTCTGTCTTCAAGGGGAAGATCTACAGAAACAAAGCGTTTCACTCT	
CTCGTGAATCCCAGAATAAGAATCCCTGCGCTGATTCAGAAAGTTCACGG	200
TATCAGCAACATGGACATCGTGGAAGCGCCAGACATGGACACAGTTTACG	
ATCTTTTCAGGGATTACGTGAAGGGAACGGTGCTCGTGTTTCACAACGCC	300
AACTTCGACCTCACTTTTCTGGATATGATGGCAAAGGAAACGGGAACTT	
TCCAATAACGAATCCCTACATCGACACACTCGATCTTTCAGAAGAGATCT	400
TTGGAAGGCCTCATTCTCTCAAATGGCTCTCCGAAAGACTTGGAATAAAA	
ACCACGATACGGCACCGTGCTCTTCCAGATGCCCTGGTGACCGCAAGAGT	500
TTTTGTGAAGCTTGTTGAATTTCTTGGTGAAAACAGGGTCAACGAATTCA	
TACGTGGAACCGGGG	567

FIG. 56

MLAMIWNDTVFCVVDTETTGTDPFAGDRIVEIAAVPVFKGKIYRNKAFHS	
LVNPRIRIPALIQKVHGISNMDIVEAPDMDTVYDLFRDYVKGTVLVFHNA	100
NFDLTFLDMMAKETGNFPITNPYIDTLDLSEEIFGRPHSLKWLSERLGIK	
TTIRHRALPDALVTARVFKLVEFLGENRVNEFIRGKRG	189

FIG. 57

GTGGAAGTTCTTTACAGGAAGTACAGGCCAAAGACTTTTTCTGAGGTTGT	
CAATCAGGATCATGTGAAGAAGGCAATAATCGGTGCTATTCAGAAGAACA	100
GCGTGGCCACGGATACATATTCGCCGGTCCGAGGGGAACGGGGAAGACT	
ACTCTTGCCAGAATTCTCGCAAATCCCTGAACTGTGAGAACAGAAAGGG	200
AGTTGAACCCTGCAATTCCTGCAGAGCCTGCAGAGAGATAGACGAGGGAA	
CCTTCATGGACGTGATAGAGCTCGACGCGGCCTCCAACAGAGGAATAGAC	300
GAGATCAGAAGAATCAGAGACGCCGTTGGATACAGGCCGATGGAAGGTAA	
ATACAAAGTCTACATAATAGACGAAGTTCACATGCTCACGAAAGAAGCCT	400
TCAACGCGCTCCTCAAAACACTCGAAGAACCTCCTTCCCACGTCGTGTTT	
GTGCTGGCAACGACAAACCTTGAGAAGGTTCTCCACGATTATCTCGAG	500
ATGTCAGGTTTTTCGAGTTCAGAAACATTCCCGACGAGCTCATCGAAAAGA	
GGCTCCAGGAAGTTGCGGAGGCTGAAGGAATAGAGATAGACAGGGAAGCT	600
CTGAGCTTCATCGCAAAAAGAGCCTCTGGAGGCTTGAGAGACGCGCTCAC	
CATGCTCGAGCAGGTGTGGAAGTTCTCGGAAGGAAAGATAGATCTCGAGA	700
CGGTACACAGGGCGCTCGGGTTGATACCGATACAGGTTGTTTCGCGATTAC	
GTGAACGCTATCTTTTCTGGTGATGTGAAAAGGGTCTTCACCGTTCTCGA	800
CGACGTCTATTACAGCGGGAAGGACTACGAGGTGCTCATTACGGAAGCAG	
TCGAGGATCTGGTCTGAAGACCTGGAAAGGGAGAGAGGGGTTTACCAGGTT	900
TCAGCGAACGATATAGTTTCAGGTTTCGAGACAACTTCTGAATCTTCTGAG	
AGAGATAAAGTTGCGCGAAGAAAAACGACTCGTCTGTAAAGTGGGTTTCGG	1000
CTTACATAGCGACGAGGTTCTCCACCACAAACGTTTACGAAAACGATGTC	
AGAGAAAAAACGATAATTCAAATGTACAGCAGAAAGAAGAGAAGAAAGA	1100
AACGGTGAAGGCAAAAGAAGAAAAACAGGAAGACAGCGAGTTTCGAGAAAC	
GCTTCAAAGAACTCATGGAAGAACTGAAAGAAAAGGGCGATCTCTCTATC	1200
TTTGTCGCTCTCAGCCTCTCAGAGGTGCAGTTTGACGGAGAAAAGGTGAT	
TATTTCTTTTGATTTCATCGAAAGCTATGCATTACGAGTTGATGAAGAAAA	1300
AACTGCCTGAGCTGGAAAACATTTTTTCTAGAAAACCTCGGGAAGAAAGTA	
GAAGTTGAACTTCGACTGATGGGAAAAGAAGAAACAATCGAGAAGGTTTC	1400
TCAGAAGATCCTGAGATTGTTTGAACAGGAGGGA	

FIG. 58

MEVLYRKYPKTFSEVVNQDHVKKAIIGAIQKNSVAHGYYIFAGPRGTGKT	
TLARILAKSLNCENRKGVEPCNSCRACREIDEGTFMDVIELDAASNRGID	100
EIRRIRDAVGYRPMEGKYKVYIIDEVHMLTKEAFNALLKTLEPPSHVVF	
VLATTNLEKVPPTIISRCQVFEFRNIPDELIEKRLQEVAAEGIEIDREA	200
LSFIAKRASGGLRDALTMLEQVWKFSEGKIDLETVHRALGLIPIQVVRDY	
VNAIFSGDVKRVFTVLDDVYYSBKDYEVLIQEAVEDLVEDLERERGVYQV	300
SANDIVQVSRQLLNLLREIKFAEEKRLVCKVGSAYIATRSTTNVQENDV	
REKNDNSNVQQKEKKETVKAKEEKQEDSEFEKRFKELMEELKEKGDLIS	400
FVALSLSEVQFDGEKVIISFDSSKAMHYELMKKKLPELENIFSRKLGKKV	
EVELRLMGKEETIEKVSQKILRLFEQEG	478

FIG. 59

ATGAAAGTAACCGTCACGACTCTTGAATTGAAAGACAAAATAACCATCGC	
CTCAAAGCGCTCGCAAAGAAATCCGTGAAACCCATTCTTGCTGGATTTCT	100
TTTTCGAAGTGAAAGATGGAAATTTCTACATCTGCGCGACCGATCTCGAG	
ACCGGAGTCAAAGCAACCGTGAATGCCGCTGAAATCTCCGGTGAGGCACG	200
TTTTGTGGTACCAGGAGATGTCATTGAGAAGATGGTCAAGGTTCTCCCAG	
ATGAGATAACGGAACCTTTCTTTAGAGGGGGATGCTCTTGTTATAAGTTCT	300
GGAAGCACCGTTTTCAGGATCACCACCATGCCCCGCGGACGAATTTCCAGA	
GATAACGCCTGCCGAGTCTGGAATAACCTTCGAAGTTGACACTTCGCTCC	400
TCGAGGAAATGGTTGAAAAGGTCATCTTCGCCGCTGCCAAAGACGAGTTC	
ATGCGAAATCTGAATGGAGTTTTCTGGGAACTCCACAAGAATCTTCTCAG	500
GCTGGTTGCAAGTGATGGTTTCAGACTTGCACTTGCTGAAGAGCAGATAG	
AAAACGAGGAAGAGGCGAGTTTCTTGCTCTCTTTGAAGAGCATGAAAGAA	600
GTTCAAACCGTGCTGGACAACACAACGGAGCCGACTATAACGGTGAGGTA	
CGATGGAAGAAGGGTTTCTCTGTCGACAAATGATGTAGAAACGGTGATGA	700
GAGTGGTCGACGCTGAATTTCCCGATTACAAAAGGGTGATCCCCGAACT	
TTCAAACGAAAGTGGTGGTTTCCAGAAAAGAACTCAGGGAATCTTTGAA	800
GAGGGTGATGGTGATTGCCAGCAAGGGAAGCGAGTCCGTGAAGTTCGAAA	
TAGAAGAAAACGTTATGAGACTTGTGAGCAAGAGCCCGATTATGGAGAA	900
GTGGTCGATGAAGTTGAAGTTCAAAAAGAAGGGGAAGATCTCGTGATCGC	
TTTCAACCCGAAGTTCATCGAGGACGTTTTGAAGCACATTGAGACTGAAG	1000
AAATCGAAATGAACTTCGTTGATTCTACCAGTCCATGTCAGATAAATCCA	
CTCGATATTTCTGGATACCTTTACATAGTGATGCCCATCAGACTGGCA	1098

FIG. 60

MKVTVTTLLELKDKITIASKALAKKSVKPILAGFLFEVKDGNFYICATDLE	
TGVKATVNAAEISGEARFVVPDVIQKMVKVLPDEITELSLEGDALVISS	100
GSTVFRITTMPADEFPEITPAESGITFEVDTSLLLEEMVEKVIFAAAKDEF	
MRNLNGVFWELHKNLLRLVASDGFRLALAEQIENEEEASFLLSLKSMKE	200
VQNVLDNTTEPTITVRYDGRRVSLSTNDVETVMRVVDAEFPDYKRVIPET	
FKTKVVVSRKELRESLKRVMVIAASKGESVKFEIEENVMLVSKSPDYGE	300
VVDEVEVQKEGEDLVIAFNPKFIEDVLKHIEETEEIEMNFVDSTSPCQINP	
LDISGYLYIVMPIRLA	366

FIG. 61

ATGCCAGTCACGTTTCTCACAGGTACTGCAGAACTCAGAAGGAAGAATT	
GATAAAGAACTCCTGAAGGATGGTAACGTGGAGTACATAAGGATCCATC	100
CGGAGGATCCCGACAAGATCGATTTTCATAAGGTCTTTACTCAGGACAAAG	
ACGATCTTTTCCAACAAGACGATCATTGACATCGTCAATTTTCGATGAGTG	200
GAAAGCACAGGAGCAGAAGCGTCTCGTTGAACTTTTGAAAAACGTACCGG	
AAGACGTTTCATATCTTCATCCGTTCTCAAAAAACAGGTGGAAAGGGAGTA	300
GCGCTGGAGCTTCCGAAGCCATGGGAAACGGACAAGTGGCTTGAGTGGAT	
AGAAAAGCGCTTCAGGGAGAATGGTTTGCTCATCGATAAAGATGCCCTTC	400
AGCTGTTTTTCTCCAAGGTTGGAACGAACGACCTGATCATAGAAAGGGAG	
ATTGAAAAACTGAAAGCTTATTCCGAGGACAGAAAGATAACGGTAGAAGA	500
CGTGGAAAGAGGTCGTTTTTACCTATCAGACTCCGGGATACGATGATTTTT	
GCTTTGCTGTTTCCGAAGGAAAAAGGAAGCTCGCTCACTCTCTTCTGTCG	600
CAGCTGTGGAAAACCAACAGAGTCCGTGGTGATTGCCACTGTCCTTGCGAA	
TCACTTCTTGGATCTCTTCAAATCCTCGTTCTTGTGACAAAGAAAAGAT	700
ACTACACCTGGCCTGATGTGTCCAGGGTGTCCAAAGAGCTGGGAATTCCC	
GTTCTCGTGTGGCTCGTTTCCTCGGTTTCTCCTTTAAGACCTGGAAATT	800
CAAGGTGATGAACCACCTCCTCTACTACGATGTGAAGAAGGTTAGAAAGA	
TACTGAGGGATCTCTACGATCTGGACAGAGCCGTGAAAAGCGAAGAAGAT	900
CCAAAACCGTTCTTCCACGAGTTCATAGAAGAGGTGGCACTGGATGTATA	
TTCTCTTCAGAGAGATGAAGAA	972

FIG. 62

MPVTFLTGTAEQKEELIKKLLKDG NVEYIRIHPEDPKIDFIRSLLR TK	
TIFSNKTIIDIVNFDEWKAQEQKRLVELLKNVPEDVHIFIRSQKTGGKGV	100
ALELPKPWETDKWLEWIEKRFRENGLLIDKDALQLFFSKVGTNDLI IERE	
IEKLKAYSEDRKITVEDVEEVFTYQTPGYDDFCFAVSEGKRKLHSLLS	200
QLWKTTESVVIATVLANHFLDLFKILVLVTKKRYTWPDVSRVSKELGIP	
VPRVARFLGFSFKTWKFKVMNHLLYYDVKKVRKILRDLYDLDRV KSEED	300
PKPFFHEFIEEVALDVYSLQRDEE	

FIG. 63

ATGAACGATTTGATCAGAAAGTACGCTAAAGATCAACTGGAAACTTTGAA	
AAGGATCATAGAAAAGTCTGAAGGAATATCCATCCTCATAAATGGAGAAG	100
ATCTCTCGTATCCGAGAGAAGTATCCCTTGAACCTCCCGAGTACGTGGAG	
AAATTTCCCCCGAAGGCCTCGGATGTTCTGGAGATAGATCCCGAGGGGGA	200
GAACATAGGCATAGACGACATCAGAACGATAAAGGACTTCCTGAACTACA	
GCCCCGAGCTCTACACGAGAAAAGTACGTGATAGTCCACGACTGTGAAAGA	300
ATGACCCAGCAGGCGGCGAACGCGTTTCTGAAGGCCCTTGAAGAACCACC	
AGAATACGCTGTGATCGTTCTGAACACTCGCCGCTGGCATTATCTACTGC	400
CGACGATAAAGAGCCGAGTGTTTCAGAGTGGTTGTGAACGTTCCAAAGGAG	
TTCAGAGATCTCGTGAAAGAGAAAATAGGAGATCTCTGGGAGGAACTTCC	500
ACTTCTTGAGAGAGACTTCAAAACGGCTCTCGAAGCCTACAACTTGGTG	
CGGAAAAACTTTCTGGATTGATGGAAAGTCTCAAAGTTTTGGAGACGGAA	600
AAACTCTTGAAAAAGGTCCTTTCAAAGGCCCTCGAAGGTTATCTCGCATG	
TAGGGAGCTCCTGGAGAGATTTTCAAAGGTGGAATCGAAGGAATTCTTTG	700
CGCTTTTTTGATCAGGTGACTAACACGATAACAGGAAAAGACGCGTTTCTT	
TTGATCCAGAGACTGACAAGAATCATTTCTCCACGAAAACACATGGGAAAG	800
CGTTGAAGATCAAAAAGCGTGTCCTTCCTCGATTCAATTCTCAGGGTGA	
AGATAGCGAATCTGAACAACAACTCACTCTGATGAACATCCTCGCGATA	900
CACAGAGAGAGAAAGAGAGGGTGTCAACGCTTGGAGC	

FIG. 64

MNDLIRKYAKDQLETLKRIIEKSEGISILINGEDLSYPREVSLELPEYVE	
KFPPKASDVLEIDPEGENIGIDDIRTIKDFLNYSPELYTRKYVIVHDCER	100
MTQQAANAFLEKALEEPPEYAVIVLNRWRHYLLPTIKSRVFRVVVNPKE	
FRDLVKEKIGDLWEELPLLERDFKTALEAYKLGAEKLSGLMESLKVLETE	200
LLKKVLSKGLEGYLACRELLERFSKVESKEFFALFDQVTNTITGKDAFL	
LIQRLTRIILHENTWESVEDKSVSFLDSILRVKIANLNNKLTLMNILAIH	300
RERKRGVNAWS	

FIG. 65

ATGTCCTTCTTCAACAAGATCATACTCATAGGAAGACTCGTGAGAGATCC	
CGAAGAGAGATACACGCTCAGCGGAACTCCAGTCACCACCTTCACCATAG	100
CGGTGGACAGGGTTCCAGAAAGAACGCGCCGGACGACGCTCAAACGACT	
GATTTCTTCAGGATCGTCACCTTTGGAAGACTGGCAGAGTTCGCTAGAAC	200
CTATCTCACCAAAGGAAGGCTCGTTCTCGTCGAAGGTGAAATGAGAATGA	
GAAGATGGGAAACACCCACTGGAGAAAAGAGGGTATCTCCGGAGGTTGTC	300
GCAAACGTTGTTAGATTGATGGACAGAAAACCTGCTGAAACAGTTAGCGA	
GACTGAAGAGGAGCTGGAAATACCGGAAGAAGACTTTTCCAGCGATACCT	400
TCAGTGAAGATGAACCACCATT	

FIG. 66

MSFFNKIILIGRLVRDPEERYTLSGTPVTTFTIAVDRVPRKNAPDDAQT	
DFFRIVTFGRLAEFARTYLTGRLVLVEGEMRMRRWETPTGEKRVSPVV	100
ANVVRFMDRKPAETVSETEEELEIPEEDFSSDTFSEDEPPF	

FIG. 67

ATGCGTGTTCCCCCGCACAACTTAGAGGCCGAAGTTGCTGTGCTCGGAAG	
CATATTGATAGATCCGTCGGTAATAAACGACGTTCTTGAAATTTTGAGCC	100
ACGAAGATTTCTATCTGAAAAACACCAACACATCTTCAGAGCGATGGAA	
GAGCTTTACGACGAAGGAAAACCGGTGGACGTGGTTTCCGTCTGTGACAA	200
GCTTCAAAGCATGGGAAAACCTCGAGGAAGTAGGTGGAGATCTGGAAGTGG	
CCCAGCTCGCTGAGGCTGTGCCAGTTCTGCACACGCACTTCACTACGCG	300
GAGATCGTCAAGGAAAAATCCATTCTGAGGAACTCATTGAGATCTCCAG	
AAAAATCTCAGAAAGTGCCTACATGGAAGAAGATGTGGAGATCCTGCTCG	400
ACAACGCAGAAAAGATGATCTTCGAGATCTCAGAGATGAAAACGACAAAA	
TCCTACGATCATCTGAGAGGCATCATGCACCGGGTGGTTTGAAAACCTGGA	500
GAACCTTCAGGGAAAGAGCCAACCTTATAGAACCCGGTGTGCTCATAACGG	
GACTACCAACGGGATTCAAAAGTCTGGACAAACAGACCACAGGGTTCAC	600
AGCTCCGATCTGGTGATAATAGCAGCGAGACCCTCCATGGGAAAAACCTC	
CTTCGCACTCTCAATAGCGAGGAACATGGCTGTCAATTTGAAATCCCCG	700
TCGGAATATTCACTCTCGAGATGTCCAAGGAACAGCTCGCTCAAAGACTA	
CTCAGCATGGAGTCCGGTGTGGATCTTTACAGCATCAGAACAGGATACCT	800
GGATCAGGAGAAGTGGGAAAGACTCACAATAGCGGCTTCTAAACTCTACA	
AAGCACCCTAGTTGTGGACGATGAGTCACTCCTCGATCCGCGATCGTTG	900
AGGGCAAAGCGAGAAGGATGAAAAAGAATACGATGTAAAAGCCATTTT	
TGTCGACTATCTCCAGCTCATGCACCTGAAAGGAAGAAAAGAAAGCAGAC	1000
AGCAGGAGATATCCGAGATCTCGAGATCTCTGAAGCTCCTTGCGAGGGAA	
CTCGACATAGTGGTGATAGCGCTTTCACAGCTTTCGAGGGCCGTAGAACA	1100
GAGAGAAGACAAAAGACCGAGGCTGAGTGACCTCAGGGAATCCGGTGCGA	
TAGAACAGGACGCAGACACAGTCATCTTCATCTACAGGGAGGAATATTAC	1200
AGGAGCAAAAAATCCAAAGAGGAAAGCAAGCTTCACGAACCTCACGAAGC	
TGAAATCATAATAGGTAAACAGAGAAACGGTCCCGTTGGAACGATCACTC	1300
TGATCTTCGACCCAGAACGGTTACGTTCCATGAAGTCGATGTGGTGCAT	
TCA	1353

FIG. 68

MRVPPHNLEAEVAVLGSILIDPSVINDVLEILSHEDFYLLKKHQHIFRAME	
ELYDEGKPDVSVCDKLQSMGKLEEVGGDLEVAQLAEAVPSSAHALHYA	100
EIVKEKSILRKLIIEISRKISESAYMEEDVEILLDNAEKMIFEISEMKTTK	
SYDHLRGIMHRVFENLENFRERANLIEPGVLITGLPTGFKSLDKQTTGFH	200
SSDLVIAARPSMGKTSFALSIARNMAVNFEIPVGIFSLEMSKEQLAQL	
LSMESGVDLYSIRTGYLDQEKWERLTIAASKLYKAPIVDDDESLLDPRSL	300
RAKARRMKKEYDVKAIFVDYLQMLHLKGRKESRQQEISEISRSCLKLLARE	
LDIVVIALSQLSRAVEQREDKRPRLSDLRESGAIEQDADTVIFIYREEYY	400
RSKKSKEESKLHEPHEAEIIIGKQRNGPVGTTITLIFDPRTVTFHEVDVVH	
S	451

FIG. 69

GTGATTCCCTCGAGAGGTCATCGAGGAAATAAAAGAAAAGGTTGACATCGT	100
AGAGGTCATTTCCGAGTACGTGAATCTTACCCGGGTAGGTTCCCTCTACA	
GGGCTCTCTGTCCCTTTCATTTCAGAAACCAATCCTTCTTTCTACGTTTCA	200
CCGGGTTTGAAGATATACCATTTGTTTCGGCTGCGGTGCGAGTGGAGACGT	
CATCAAATTTCTTCAAGAAATGGAAGGGATCAGTTTCCAGGAAGCGCTGG	300
AAAGACTTGCCAAAAGAGCTGGGATTGATCTTTCTCTCTACAGAACAGAA	
GGGACTTCTGAATACGGAAAATACATTTCGTTTGTACGAAGAAACGTGGAA	400
AAGGTACGTCAAAGAGCTGGAGAAATCGAAAGAGGCCAAAAGACTATTTAA	
AAAGCAGAGGCTTCTCTGAAGAAGATATAGCAAAGTTTCGGCTTTGGGTAC	500
GTCCCCAAGAGATCCAGCATCTCTATAGAAGTTGCAGAAGGCATGAACAT	
AACACTGGAAGAACTTGTTCAGATACGGTATCGCGCTGAAAAAGGGTGATC	600
GATTTCGTTGATAGATTTCGAAGGAAGAATCGTTGTTCCAATAAAGAACGAC	
AGTGGTCATATTGTGGCTTTTGGTGGGCGTGCTCTCGGCAACGAAGAACC	700
GAAGTATTTGAACTCTCCAGAGACCAGGTATTTTTCGAAGAAGAAGACCC	
TTTTTCTCTTCGATGAGGCGAAAAAGTGGCAAAAGAGGTTGGTTTTTTC	800
GTCATCACCGAAGGCTACTTCGACGCGCTCGCATTTCAGAAAGGATGGAAT	
ACCAACGGCGGTGCTGTTCTTGGGGCGAGTCTTCAAGAGAGGCGATTTC	900
TAAACTTTTCGGCGTATTCGAAAAACGTCATACTGTGTTTCGATAATGAC	
AAAGCAGGCTTCAGAGCCACTCTCAAATCCCTCGAGGATCTCCTAGACTA	1000
CGAATTCAACGTGCTTGTGGCAACCCCTCTCCTTACAAAGACCCAGATG	
AACTCTTTCAGAAAGAAGGAGAAGGTTTCATTGAAAAAGATGCTGAAAAAC	1100
TCGCGTTCGTTTCGAATATTTTCTGGTGACGGCTGGTGAGGTCTTCTTTGA	
CAGGAACAGCCCCGCGGGTGTGAGATCCTACCTTTCTTTCCTCAAAGGTT	1200
GGGTCCAAAAGATGAGAAGGAAAGGATATTTGAAACACATAGAAAATCTC	
GTGAATGAGGTTTCATCTTCTCTCCAGATACCAGAAAACCAGATTTTGAA	1300
CTTTTTTTGAAAGCGACAGGTCTAACACTATGCCTGTTTCATGAGACCAAGT	
CGTCAAAGGTTTACGATGAGGGGAGAGGACTGGCTTATTTGTTTTTTGAAC	1400
TACGAGGATTTGAGGGAAAAGATTCTGGAAGTGGACTTAGAGGTACTGGA	
AGATAAAAACGCGAGGGAGTTTTTCAAGAGAGTCTCACTGGGAGAAGATT	1500
TGAACAAAGTCATAGAAAACCTCCCAAAGAGCTGAAAGACTGGATTTTTT	
GAGACAATAGAAAGCATTCCTCCTCCAAAGGATCCCGAGAAATTCCTCGG	1600
TGACCTCTCCGAAAAGTTGAAAATCCGACGGATAGAGAGACGTATCGCAG	
AAATAGATGATATGATAAAGAAAGCTTCAAACGATGAAGAAAGGCGTCTT	1695
CTTCTCTCTATGAAAGTGATCTCCTCAGAAAAATAAAGAGGAGG	

FIG. 70

MIPREVIEEIKEKVDIVEVISEYVNLTRVGSSYRALCPFHSETNPSFYVH	
PGLKIYHCFGCGASGDVIKFLQEMEGISFQEALERLAKRAGIDLSLYRTE	100
GTSEYGKYIRLYEETWKRYVKELEKSKEAKDYLSRGFSEEDIAKFGFGY	
VPKRSSISIEVAEGMNITLEELVRYGIALKKGDRFVDRFEGRIVVPIKND	200
SGHIVAFGGRALGNEEPKYLNSPETRYFSKKKTFLFLFDEAKKVAKEVGFF	
VITEGYFDALAFRKDGIPTAVAVLGASLSREAILKLSAYSKNVILCFDND	300
KAGFRATLKSLEDLLDYEFNVLVATPSPYKDPDELFOKEGEGSLKKMLKN	
SRSFEYFLVTAGEVFFDRNSPAGVRSYLSFLKGWVQKMRRKGYLKHIEENL	400
VNEVSSSLQIPENQILNFFESDRSNTMPVHETKSSKVYDEGRGLAYLFLN	
YEDLRKILELDLEVLEDKNAREFFKRVSLGEDLNKVIENFPKELKDWIF	500
ETIESIPPPKDPEKFLGDLSEKLKIRRIERRIAEIDDMIKKASNDEERRL	
LLSMKVDLLRKIKRR	565

FIG. 71

ATGGCTCTACACCGGCTCACCCTGGGGCAATAATCGGGCACGAGGCCGT	
TCTCGCCCTCCTTCCCCGCCTCACCGCCAGACCCTGCTCTTCTCCGGCC	100
CCGAGGGGGTGGGGCGGCGCACCGTGGCCCGCTGGTACGCTGGGGGCTC	
AACCGCGGCTTCCCCCGCCCTCCCTGGGGGAGCACCGGACGTCCTCGA	200
GGTGGGGCCCAAGGCCCGGGACCTCCGGGGCCGGGCCGAGGTGCGGCTGG	
AGGAGGTGGCGCCCCCTCTTGAGTGGTGCTCCAGCCACCCCCGGGAGCGG	300
GTGAAGGTGGCCATCCTGGACTCGGCCCACCTCCTCACCGAGGCCGCCGC	
CAACGCCCTCCTCAAGCTCCTGGAGGAGCCCCCTTCTACGCCCGCATCG	400
TCCTCATCGCCCCAAGCCGCGCCACCCTCCTCCCCACCCTGGCCTCCCGG	
GCCACGGAGGTGGCATTCGCCCCCGTGCCCGAGGAGGCCCTGCGCGCCCT	500
CACCCAGGACCCGGAGCTCCTCCGCTACGCCCGCGGGGCCCCGGGCCGCC	
TCCTTAGGGCCCTCCAGGACCCGGAGGGGTACCGGGCCCGCATGGCCAGG	600
GCGCAAAGGGTCTTGAAAGCCCCGCCCTGGAGCGCCTCGCTTTGCTTCG	
GGAGCTTTTGGCCGAGGAGGAGGGGGTCCACGCCCTCCACGCCGTCCTAA	700
AGCGCCCGGAGCACCTCCTTGCCCTGGAGCGGGCGCGGGAGGCCCTGGAG	
GGGTACGTGAGCCCCGAGCTGGTCCTCGCCCGGCTGGCCTTAGACTTAGA	800
GACA	

FIG. 72

MALHPAHPGAIIGHEAVLALLPRLTAQTLLFSGPEGVGRRTVARWYAWGL	
NRGFPPPSLGEHPDVLEVGPKARDLRGRAEVRLEEVAPLLEWCSSHPRER	100
VKVAILDSAHLLEAAANALLKLEEPSYARIVLIAPSRATLLPTLASR	
ATEVAFAPVPEEALRALTQDPELLRYAAGAPGRLLRALQDPEGYRARMAR	200
AQRVLKAPPLERLALLRELLAEEEGVHALHAVLKRPEHLLALERAREALE	
GYVSPELVLARLALDLET	268

FIG. 73

ATGCTGGACCTGAGGGAGGTGGGGGAGGCGGAGTGGAAGGCCCTAAAGCC	
CCTTTTGGAAGCGTGCCCGAGGGCGTCCCCGTCTCCTCCTGGACCCTA	100
AGCCAAGCCCCTCCCGGGCGGCCTTCTACCGGAACCGGGAAGGCGGGAC	
TTCCCCACCCCCAAGGGGAAGGACCTGGTGCGGCACCTGGAAAACCGGGC	200
CAAGCGCCTGGGGCTCAGGCTCCCGGGCGGGGTGGCCAGTACCTGGCCT	
CCCTGGAGGGGGACCTCGAGGCCCTGGAGCGGGAGCTGGAGAAGCTTGCC	300
CTCCTCTCCCCACCCCTCACCCCTGGAGAAGGTGGAGAAGGTGGTGGCCCT	
GAGGCCCCCCTCACGGGCTTTGACCTGGTGCGCTCCGTCTCTGGAGAAGG	400
ACCCAAGGAGGCCCTCCTGCGCCTAGGCGGCCTCAAGGAGGAGGGGGAG	
GAGCCCCTCAGGCTCCTCGGGGCCCTCTCCTGGCAGTTGCCCCCTCCTCGC	500
CGGGGCCTTCTTCTCCTCCTCGGGGAAAACCCAGGCCCAAGGAGGAGGACC	
TCGCCCCGCTCGAGGCCACCCCTACGCCGCCCGCCGCGCCCTGGAGGCG	600
GCGAAGCGCCTCACGGAAGAGGCCCTCAAGGAGGCCCTGGACGCCCTCAT	
GGAGGCGGAAAAGAGGGCCAAGGGGGGGAAGACCCGTGGCTCGCCCTGG	700
AGGCGGCGGTCTCTCCGCCTCGCCCGTTGA	

FIG. 74

MVIAFTGDPFLAREALLEEARLRGLSRFTEPTPEALAQALAPGLFGGGGA	
MLDLREVGEAEWKALKPLLESVPEGVPVLLLDPKPSPSRAAFYRNRRRD	100
FPTPKGKDLVRHLENRAKRLGLRLPGGVAQYLASLEGDLEALERELEKLA	
LLSPPLTLEKVEKVVALRPPLTGFDLVRVLEKDPKEALLRLGGLKEEGE	200
EPLRLLGALSWQFALLARAFFLLRENPRPKEEDLARLEAHPYAARRALEA	
AKRLTEEALKEALDALMEAEKRAKGKDPWLALAAVLRRLAR	292

FIG. 75

ATGGCTCGAGGCCTGAACCGCGTTTTCTCATCGGCGCCCTCGCCACCCG	
GCCGGACATGCGCTACACCCGGCGGGGCTCGCCATTTTGGACCTGACCC	100
TCGCCGGTCAGGACCTGCTTCTTTCCGATAACGGGGGGGAACCGGAGGTG	
TCCTGGTACCACCGGGTGAGGCTCTTAGGCCGCCAGGCGGAGATGTGGGG	200
CGACCTCTTGGAACCAAGGGCAGCTCGTCTTCGTGGAGGGCCGCCTGGAGT	
ACCGCCAGTGGGAAAGGGAGGGGGAGAAGCGGAGCGAGCTCCAGATCCGG	300
GCCGACTTCCGGACCCCTGGACGACCGGGGGAAGAAGCGGGCGGAGGAC	
AGCCGGGGCCAGCCAGGCTCCGCGCCGCCCTGAACCAGGTCTTCCTCAT	400
GGGCAACCTGACCCGGGACCCGGAACCTCCGCTACACCCCCAGGGGCACCG	
CGGTGGCCCGGCTGGGCTGGCGGTGAACGAGCGCCGC CAGGGGGCGGAG	500
GAGCGCACCCACTTCGTGGAGGTT CAGGCCTGGCGCGA CCTGGCGGAGTG	
GGCCGCCGAGCTGAGGAAGGGCGACGGCCTTTTCGTGATCGGCAGGTTGG	600
TGAACGACTCCTGGACCAGCTCCAGCGGCGAGCGGCGCTTCCAGACCCGT	
GTGGAGGCCCTCAGGCTGGAGCGCCCCACCCGTGGACCTGCCCAGGCCTG	700
CCCAGGCCGGCGGAACAGGTCCCGCGAAGTCCAGACGGGTGGGGTGGACA	
TTGACGAAGGCTTGGAAGACTTCCGCGGAGGAGGATTTGCCGTTTTGA	800
GCACGAA	

FIG. 76

MARGLNRVFLIGALATRPDMRYTPAGLAILDLTLAQDLLLLSDNGGEPEV	
SWYHRVRLGRQAEMWGDLLDQGQLVFVEGRLEYRQWEREGEKRSELQIR	100
ADFLDPLDDRGGKKRAEDSRGQPRRLRAALNQVFLMGNLTRDPELRYTPQGT	
AVARLGLAVNERRQGAERTHFVEVQAWRDLAEWAAELRKGDGLFVIGRL	200
VNDSWTSSSGERRFQTRVEALRLERPTRGPAQACPGRRNRSREVQTGGVD	
IDEGLEDFPPEEDLPF	266

FIG. 77

AATTCCGACATTTCAATTGAATCGTTTATTCCGCTTGAAAAAGAAGGCAA	
GTTGCTCGTTGATGTGAAAAGACCGGGGAGCATCGTACTGCAGGCGCGCT	100
TTTTCTCTGAAATCGTGAAAAAAGTCCGCAACAAACGGTGGAATCGAA	
ACGGAAGACAACCTTTTTGACGATCATCCGCTCGGGGCACTCAGAATTCGG	200
CCTCAATGGGCTAAACGCCGACGAATATCCGCGCCTGCCGCAAATTGAAG	
AAGAAAACGTGTTTCAAATCCCGGCTGATTTATTGAAAACCGTGATTTCGG	300
CAAACGGTGTTTCGCCGTTTCTACATCGGAAACGCGCCCAATCTTGACAGG	
TGTCAACTGGAAAGTTGAACATGGCGAGCTTGTCTGCACAGCGACCGACA	400
GTCAATCGCTTAGCCATGCGCAAAGTGAAAATTGAGTCGGAAAATGAAGTA	
TCATACAACGTCGTCATCCCTGGAAAAAGTCTTAATGAGCTCAGCAAAAT	500
TTTGGATGACGGCAACCACCCGGTGGACATCGTCATGACAGCCAATCAAG	
TGCTATTTAAGGCCGAGCACCTTCTCTTCTTTCCCGGCTGCTTGACGGC	600
AACTATCCGGAGACGGCCCGCTTGATTCCAACAGAAAGCAAAACGACCAT	
GATCGTCAATGCAAAAGAGTTTCTGCAGGCAATCGACCGAGCGTCCTTGC	700
TTGCTCGAGAAGGAAGGAACAACGTTGTGAAACTGACGACGCTTCCTGGA	
GGAATGCTCGAAATTTCTTCGATTTCTCCGAGATCGGGAAAGTGACGGAG	800
CAGCTGCAAACGGAGTCTCTTGAAGGGGAAGAGTTGAACATTTCTGTTTCA	
CGCGAAATATATGATGGACGCGTTGCGGGCGCTTGATGGAACAGACATTT	900
CAAATCAGCTTCACTGGGGCCATGCGGCCGTTCTGTTGCGCCCGCTTCA	
ACCGATTCGATGCTTCAGCTCATTTTGCCGGTGAGAACATAT	992

FIG. 78

NSDISIIIESFIPLEKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEI	
ETEDNFLTIIIRSGHSEFRLNGLNADEYPRLPQIEEENVFQIPADLLKTVI	100
RQTVFAVSTSETRPILTGVDNWKVEHGELVCTATDSHRLAMRKVKII ESEN	
EVSYNVVIPGKSLNELSKII LDDGNHPVDIVMTANQVLFKAEHLLFFSRL	200
LDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLT	
LPGGMLEISSISPEIGKVTEQLQTESLEGEELNISFS AKYMMDALRALDG	300
TDIQISFTGAMRPFLLRPLHTDSMLQLILPVRTY	

FIG. 79

ATGATTAACCGCGTCATTTTGGTCGGCAGGTTAACGAGAGATCCGGAGTT	
GCGTTACACTCCAAGCGGAGTGGCTGTTGCCACGTTTACGCTCGCGGTCA	100
ACCGTCCGTTTACAAATCAGCAGGGCGAGCGGGAAACGGATTTTATTCAA	
TGTGTCGTTTGGCGCCGCCAGGCGGAAAACGTCGCCAACTTTTTGAAAAA	200
GGGGAGCTTGGCTGGTGTTCGATGGCCGACTGCAAACCCGCAGCTATGAAA	
ATCAAGAAGGTCGGCGTGTGTACGTGACGGAAGTGGTGGCTGATAGCGTC	300
CAATTTCTTGAGCCGAAAGGAACGAGCGAGCAGCGAGGGGCGACAGCAGG	
CGGCTACTATGGGGATCCATTCCCATTCTGGGCAAGATCAGAACCACCAAT	400
ATCCGAACGAAAAAGGGTTTGGCCGCATCGATGACGATCCTTTCGCCAAT	
GACGGCCAGCCGATCGATATTTCTGATGATGATTTGCCGTTT	492

FIG. 80

MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRRV	
YVTEVVADSVQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRRQAEN	100
VANFLKKGSLAGVDGRLQTRGDPFPFGQDQNHQYPNEKGFGRIDDDPFAN	
DGQPIDISDDDLPF	164

FIG. 81

ATGCTGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCCT	
TTATTTATTATACGGCAATGAGCCGTTTTTATTAACGGAAACGTATGAGC	100
GATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAACCTTGGCT	
GTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGGCCGA	200
GACGGTGCCGTTTTTTCGGCGAGCGGCGTGTCAATTCTCATCAAGCATCCAT	
ATTTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTGGCGAAG	300
CTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCTTTTT	
CGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTCGCCA	400
AAGAGCAAAGCGAAGTCGTCATCGCCGCCCGCTCGCCGAAGCGGAGCTG	
CGTGCCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAGCAAGCGA	500
CGAGGCGATTGATGTCCTGTTGCGGCGGGCCGGGACGCAGCTTCCGCCT	
TGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCGGATCGGGCGGAACC	600
ATCGAGGCGGCGGCGGTTGAGCGGCTTGTGCCCGCACGCCGGAAGAAAA	
CGTATTTGTGCTTGTGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT	700
TGCAGACGTTTTATGATCTGCTTGAAAACAATGAAGAGCCGATCAAATT	
TTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTTCGCAAGTGAAATGGCT	800
TGCCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGC	
ACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCCGCTTCGCTGAC	900
GGAGAGCTTGCTGAGGCGATCAACGAGCTCGCTGACGCCGATTACGAAGT	
GAAAGCGGGGCGGTCGATCGCCGTTGGCCGTTGAGCTGCTTCTGATGC	1000
GCTGGGGCGCCCCGCCGCGCAAGCGGGGCGCCACGGCCGGCGG	

FIG. 82

MLERVWGNIEKRRFSPLYLLYGNEPFLLTETYERLVNAALGPEEREWNLA	
VYDCEETPIEAALAEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAK	100
LEAYLKAPSPFSIVVFFAPYEKLDERKKITKLAKQSEVVIAAPLAEAL	
RAWVRRRIESQGAQASDEAIDVLLRRAGTQLSALANEIDKLALFAGSGGT	200
IEAAAVERLVARTPEENVFVLVEQVAKRDI PAALQTFYDLLENNEEPIKI	
LALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD	300
GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHR	

FIG. 83

ATGCGATGGGAACAGCTAGCGAAACGCCAGCCGGTGGTGGCGAAAATGCT	
GCAAAGCGGCTTGGA AAAAGGGCGGATTTCTCATGCGTACTTGTTTGAGG	100
GGCAGCGGGGGACGGGCAAAAAGCGGCCAGTTTGTGTTGGCGAAACGT	
TTGTTTTGTCTGTCCCAATCGGAGTTTCCCGTGTCTAGAGTGCCGCAA	200
CTGCCGGCGCATCGACTCCGGCAACCACCCTGACGTCCGGGTGATCGGCC	
CAGATGGAGGATCAATCAAAAAGGAACAAATCGAATGGCTGCAGCAAGAG	300
TTCTCGAAAACAGCGGTGCGAGTCGGATAAAAAAATGTACATCGTTGAGCA	
CGCCGATCAAATGACGACAAGCGCTGCCAACAGCCTTCTGAAATTTTGG	400
AAGAGCCGCATCCGGGGACGGTGGCGGTATTGCTGACTGAGCAATACCAC	
CGCTTGCTAGGGACGATCGTTTCCCGTGTCAAGTGCTTTCGTTCCGGCC	500
GTTGCCGCCGGCAGAGCTCGCCCAGGGACTTGTCGAGGAGCACGTGCCGT	
TGCCGTTGGCGCTGTTGGCTGCCCATTTGACAAACAGCTTCGAGGAAGCA	600
CTGGCGCTTGCCAAAGATAGTTGGTTTGCCGAGGCGCGAACATTAGTGCT	
ACAATGGTATGAGATGCTGGGCAAGCCGGAGCTGCAGCTTTTGTTTTTCA	700
TCCACGACCGCTTGTTTCCGCATTTTTTGAAAGCCATCAGCTTGACCTT	
GGACTTG	757

FIG. 84

MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRTGKKAASLLLA KR	
LFCLSPIGVSPCLECRNCRRIDSGNHPDVRVIGPDGGS IKKEQIEWLQQE	100
FSKTAVESDKKMYIVEHADQMTTSAANSLLKFLEEPHPGTVAVLLTEQYH	
RLLGTIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA	200
LALAKDSWFAEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL	
GL	252

FIG. 85

GTGGCATAACCAAGCGTTATATCGCGTGTTTCGGCCGCAGCGCTTTGCGGA	
CATGGTCGGCCAAGAACACGTGACCAAGACGTTGCAAAGCGCCCTGCTTC	100
AACATAAAATATCGCACGCTTACTTATTTTCCGGCCCGCGCGGTACAGGA	
AAAACGAGCGCGAGCGAAAATTTTCGCCAAGGCGGTCAACTGTGAACAGGC	200
GCCAGCGGCGGAGCCATGCAATGAGTGTCCAGCTTGCCTCGGCATTACGA	
ATGGAACGGTTCCTCGATGTGCTGGAAATTGACGCTGCTTCCAACAACCGC	300
GTCGATGAAATTCGTGATATCCGTGAGAAGGTGAAATTTGCGCCAACGTC	
GGCCCGCTACAAAGTGTATATCATCGACGAGGTGCATATGCTGTGATCG	400
GTGCGTTTAAACGCGCTGTTGAAAACGTTGGAGGAGCCGCCGAAACACGTC	
ATTTTCATTTTGGCCACGACCGAGCCGCACAAAATTCCGGCGACGATCAT	500
TTCCCGCTGCCAACGGTTCGATTTTCGCCGCATCCCGCTTCAGGCGATCG	
TTTCACGGCTAAAGTACGTGCAAGCGCCCAAGGTGTCGAGGCGTCAGAT	600
GAGGCATTGTCCGCCATCGCCCGTGCTGCAGACGGGGGGATGCGCGATGC	
GCTCAGCTTGCTTGATCAAGCCATTTCTTCAGCGACGGGAAACTTCGGC	700
TCGACGACGTGCTGGCGATGACCGGGGCTGCATCATTTGCCGCCTTATCG	
AGCTTCATCGAAGCCATCCACCGCAAAGATACAGCGGCGGTTCTTCAGCA	800
CTTGGAACGATGATGGCGCAAGGGAAAGATCCGCATCGTTTGGTTGAAG	
ACTTGATTTTGTACTATCGCGATTTATTGCTGTACAAAACCGCTCCCTAT	900
GTGGAGGGAGCGATTCAAATTGCTGTGCTTGACGAAGCGTTCACTTCACT	
GTCGGAAATGATTCCGGTTTCCAATTTATACGAGGCCATCGAGTTGCTGA	1000
ACAAAAGCCAGCAAGAGATGAAGTGGACAAACCACCCGCGCCTTCTGTTG	
GAAGTGGCGCTTGTGAAACTTTGCCATCCATCAGCCGCCGCCCGTCGCT	1100
GTCGGCTTCCGAGTTGGAACCGTTGATAAAGCGGATTGAAACGCTGGAGG	
CGGAATTGCGGCGCCTGAAGGAACAACCGCCTGCCCTCCGTCGACCGCC	1200
GCGCCGGTGAAAAAACTGTCAAACCGATGAAAACGGGGGGATATAAAGC	
CCCGGTTGGCCGCATTTACGAGCTGTTGAAACAGGCGACGCATGAAGATT	1300
TAGCTTTGGTGAAAGGATGCTGGGCGGATGTGCTCGACACGTTGAAACGG	
CAGCATAAAGTGTGCGACGCTGCCTTGCTGCAAGAGAGCGAGCCGGTTGC	1400
AGCGAGCGCCTCAGCGTTTGTATTAAATTCAAATACGAAATCCACTGCA	
AAATGGCGACCGATCCCAAGTTCGGTCAAAGAAAACGTGGAAGCGATT	1500
TTGTTTGAGCTGACAAACCGCCGCTTTGAAATGGTAGCCATTCCGGAGGG	
AGAATGGGGAAAAATAAGAGAAGAGTTCATCCGCAATAAGGACGCCATGG	1600
TGGAAAAAAGCGAAGAAGATCCGTTAATCGCCGAAGCGAAGCGGCTGTTT	
GGCGAAGAGCTGATCGAAATTAAAGAA	1677

FIG. 86

VAYQALYRVFRPQRFADMVGQEHVTKTLQSALLQHKISHAYLFSGPRGTG	
KTSAAKIFAKAVNCEQAPAAEPCNECPACLGITNGTVPDVLEIDAASNNR	100
VDEIRDIREKVKFAPTSARYKVYIIDEVHMLSIGAFNALLKTLEPPKHV	
IFILATTEPHKIPATIIISRCQRFDFRRIPLQAIVSRLKYVASAQGVEASD	200
EALSAIARAADGGMRDALSLLDQAISFSDGKLRLDDVLAMTGAASFAALS	
SFIEAIHRKDTAAVLQHLETMMAQGGKDPHRLVEDLILYYRDLILLYKTAPY	300
VEGAIQIAVVDEAFTSLSEMI PVSNLYEAEI LLNKSQQEMKWTNHPRLLL	
EVALVKLCHPSAAAPSL SASELEPLIKRIETLEAELRRLKEQPPAPPSTA	400
APVKLSKPMKTGGYKAPVGRIYELLKQATHEDLALVKG CWADVLDTLKR	
QHKVSHAALLQESEPVAASASAFVLKFKYEIHCKMATDPTSSVKENVEAI	500
LFELTNRRFEMVAIPEGEWGKIREEFIRNKDAMVEKSEEDPLIAEAKRLF	
GEELIEIKE	559

FIG. 87

ATGGTGACAAAAGAGCAAAAAGAGCGGTTTCTCATCCTGCTTGAGCAGCT	100
GAAGATGACGTCGGACGAATGGATGCCGCATTTTCGTGAGGCAGCCATTC	
GCAAAGTCGTGATCGATAAAGAGGAGAAAAGCTGGCATTTTTATTTTCAG	200
TTCGACAACGTGCTGCCGGTTCATGTATACAAAACGTTTGCCGATCGGCT	
GCAGACGGCGTTCCGCCATATCGCCGCCGTCCGCCATACGATGGAGGTCTG	300
AAGCGCCGCGCGTAACCTGAGGCGGATGTGCAGGCGTATTGGCCGCTTTGC	
CTTGCCGAGCTGCAAGAAGGCATGTCGCCGCTTGTCGATTGGCTCAGCCG	400
GCAGACGCCTGAGCTGAAAGGAAACAAGCTGCTTGTCGTTGCCCGCCATG	
AAGCGGAAGCGCTGGCGATCAAACGGCGGTTTCGCCAAAAAATCGCTGAT	500
GTGTACGCTTCGTTTGGGTTTCCCCCCTTCAGCTTGACGTCAGCGTCGA	
GCCGTCCAAGCAAGAAATGGAACAGTTTTTTGCGCAAAAACAGCAAGAGG	600
ACGAAGAGCGAGCGCTTGCTGTACTGACCGATTTAGCGAGGGAAGAAGAA	
AAGGCCGCGTCTGCGCCGCCGTCCGGTCCGCTTGTCATCGGCTATCCGAT	700
CCGCGACGAGGAGCCGGTGCGGCGGGCTTGAAACGATCGTCGAAGAAGAGC	
GGCGCGTCGTTGTGCAAGGCTATGTATTTGACGCCGAAGTGAGCGAATTA	800
AAAAGCGGCCGCACGCTGTTGACCATGAAAATCACAGATTACACGAATCTC	
GATTTTAGTCAAAATGTTCTCGCGCGACAAAGAGGACGCCGAGCTTATGA	900
GCGGCGTCAAAAAGGCATGTGGGTGAAAGTGCGCGGCAGCGTGCAAAAC	
GATACGTTTCGTCCGTGATTTGGTCATCATCGCCAACGATTTGAACGAAAT	1000
CGCCGCAAACGAACGGCAAGATACGGCGCCGGAAGGGGAAAAGAGGGTCTG	
AGCTCCATTTGCATACCCCGATGAGCCAAATGGACGCGGTACCTCGGTG	1100
ACAAACTCATTGAGCAAGCGAAAAAATGGGGGCATCCGGCGATCGCCGT	
CACCGACCATGCCGTTGTTCAAGTCGTTTCCGGAGGCCTACAGCGCGGCGA	1200
AAAACACGGCATGAAGGTCATTTACGGCCTTGAGGCGAACATCGTCGAC	
GATGGCGTGCCGATCGCCTACAATGAGACGCACCGCCGTCTTTCGGAGGA	1300
AACGTACGTCGTCTTTGACGTCGAGACGACGGGCCTGTCGGCTGTGTACA	
ATACGATCATTGAGCTGGCGGCGGTGAAAGTGAAAGACGGCGAGATCATC	1400
GACCGATTTCATGTCGTTTGCCAACCCTGGACATCCGTTGTCGGTGACAAC	
GATGGAGCTGACTGGGATCACCGATGAGATGGTGAAAGACGCCCCGAAGC	1500
CGGACGAGGTGCTAGCCCGTTTTGTTGACTGGGCCGGCGATGCGACGCTT	
GTTGCCACACGCCAGCTTTGACATCGGTTTTTTAAACGCGGGCCTCGC	1600
TCGCATGGGGCGCGGCAAAATCGCGAATCCAGTCATCGATACGCTCGAGC	
TGGCCCGTTTTTTATACCCGGATTTGAAAAACCATCGGCTCAATACATTG	1700
TGCAAAAATTTGACATTGAATTGACGCAGCATACCGCGCCATCTACGA	
CGCGGAGGCGACCGGGCATTGCTTATGCGGCTGTTGAAGGAAGCGGAAG	1800
AGCGCGGCATACTGTTTCATGACGAATTAAACAGCCGCACGCACAGCGAA	
GCGTCCTATCGGCTTGCGCGCCCGTTCATGTGACGCTGTTGGCGCAAAA	1900
CGAGACTGGATTGAAAAATTTGTTCAAGCTTGTCGTCATTGTGCGACATTC	
AATATTTTACCCTGTGCGCGCATCCCGCGCTCCGTGCTCGTCAAGCAC	2000
CGCGACGGCCTGCTTGTCGGCTCGGGCTGCGACAAAGGAGAGCTGTTTGA	
CAACTTGATCCAAAAGGCGCCGGAAGAAGTCGAAGACATCGCCCGTTTTT	2100
ACGATTTTCTTGAAGTGCATCCGCCGACGTGTACAAGCCGCTCATCGAG	
ATGGATTATGTGAAAGACGAAGAGATGATCAAAAACATCATCCGCAGCAT	2200
CGTCGCCCTTGGTGAGAAGCTTGACATCCCGGTTGTCGCCACTGGCAACG	

FIG. 88A

TCCATTACTTGAACCCAGAAGATAAAATTTACCGGAAAATCTTAATCCAT	
TCGCAAGGCGGGGCGAATCCGCTCAACCGCCATGAACTGCCGGATGTATA	2 300
TTTCCGTACGACGAATGAAATGCTTGACTGCTTCTCGTTTTTATGGGCCGG	
AAAAAGCGAAGGAAATCGTCGTTGACAACACGCAAAAAATCGCTTCGTTA	2 400
ATCGGCGATGTCAAGCCGATCAAAGATGAGCTGTATACGCCGCGCATTGA	
AGGGGCGGACGAGGAAATCAGGGAAATGAGCTACCGGCGGGCGAAGGAAA	2 500
TTTACGGCGACCCGTTGCCGAAACTTGTTGAAGAGCGGCTTGAGAAGGAG	
CTAAAAGCATCATCGGCCATGGCTTTGCCGTCATTTATTTGATCTCGCA	2 600
CAAGCTTGTGAAAAAATCGCTCGATGACGGCTACCTTGTCGGGTTCGCGCG	
GATCGGTTCGGCTCGTCGTTTGTGCGGACGATGACGGAAATCACCGAGGTC	2 700
AATCCGCTGCCGCCGCATTACGTTTGCCCGAACTGCAAGCATTTCGGAGTT	
CTTTAACGACGGTTCAGTCGGCTCAGGGTTTGATTGCCGGATAAAAACT	2 800
GCCCGCGATGTGGGACGAAATACAAGAAAGACGGGCACGACATCCCGTTT	
GAGACGTTTCTCGGCTTTAAAGGCGACAAAGTGCCGGATATCGACTTGAA	2 900
CTTTTCCGGCGAATACCAGCCGCGCGCCCACTATAAGAAAGTGCTGT	
TTGGCGAAGACAACGTCTACCGCGCCGGGACGATTGGCACGGTCGCTGAC	3 000
AAAACGGCGTACGGATTTGTCAAAGCGTATGCGAGCGACCATAACTTAGA	
GCTGCGCGGCGCGGAAATCGACGGCTCGCGGCTGGCTGCACCGGGGTGAA	3 100
GCGGACGACCGGGCAGCATCCGGGCGGCATCATCGTCGTCGCCGATTATA	
TGGAATTTACGATTTTACGCCGATTCAATATCCGGCCGATGACACGTCC	3 200
TCTGAATGGCGGACGACCCATTTCTGACTTCCATTTCGATCCACGACAATTT	
GTTGAAGCTCGATATTCTCGGGCAGCAGCATCCGACGGTCATTTCGCATGC	3 300
TGCAAGATTTAAGCGGCATCGATCCGAAAACGATCCCGACCGACGACCCG	
GATGTGATGGGCATTTTCAGCAGCACCGAGCCGCTTGGCGTTACGCCGGA	3 400
GCAAATCATGTGCAATGTCGGCACGATCGGCATTCCGGAGTTTGGCACGC	
GCTTCGTTTCGGCAAATGTTGGAAGAGACAAGGCCAAAAACGTTTTCCGAA	3 500
CTCGTGCAAATTTCCGGCTTGTGCGACGGCACCGATGTGTGGCTCGGCAA	
CGCGCAAGAGCTCATTCAAAACGGCACGTGTACGTTATCGGAAGTCATCG	3 600
GCTGCCGCGACGACATTATGGTCTATTTGATTTACCGCGGGCTCGAGCCG	
TCGCTCGCTTTTAAAATCATGGAATCCGTGCGCAAAGGAAAAGGCTTAAC	3 700
GCCGGAGTTTGAAGCAGAAATGCGCAAACATGACGTGCCGGAGTGGTACA	
TCGATTCATGCAAAAAAATCAAGTACATGTTCCCGAAAGCGCACGCCGCC	3 800
GCCTACGTGTTAATGGCGGTGCGCATCGCCTACTTTAAGGTGCACCATCC	
GCTTTTGTATTACGCGTCGTAATTTACGGTGCGGGCGGAGGACTTTGACC	3 900
TTGACGCCATGATCAAAGGATCACCCGCCATTTCGCAAGCGGATTGAGGAA	
ATCAACGCCAAAGGCATTTCAGGCGACGGCGAAAGAAAAAGCTTGCTCAC	4 000
GGTTCTTGAGGTGGCCTTAGAGATGTGCGAGCGCGGCTTTTCCTTTAAA	
ATATCGATTTGTACCGCTCGCAGGCGACGGAATTCGTCATTGACGGCAAT	4 100
TCTCTATTCCGCCGTTCAACGCCATTCCGGGGCTTGGGACGAACGTGGC	
GCAGGCGATCGTGCGCGCCCGCGAGGAAGGCGAGTTTTTGTGCAAGGAGG	4 200
ATTTGCAACAGCGCGGCAAATTGTGCAAAACGCTGCTCGAGTATCTAGAA	
AGCCGCGGCTGCCTTGACTCGCTTCCAGACCATAACCAGCTGTGCTGTT	4 300

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FIG. 88B

MVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHFFQ	
FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLC	100
LAELQEGMSPLVDWLSRQTPELKGNKLLVVARHEAEALAIKRRFAKKIAD	
VYASFGFPPLQLDVSVEPSKQEMEQLAQKQQEDEERALAVLTDLAREEE	200
KAASAPPSGPLVIGYPIDEEPVRRLLETIVEEERRVVVQGYVFDAEVSEL	
KSGRTLTLTKITDYTNSILVKMFSRDKEDAELMSGVKKGMWVKVRSVQN	300
DTFVRDLVIIANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV	
TKLIEQAKKWGHPAIAVTDHAVVQSFPEAYSAAKKHGMKVIYGLEANIVD	400
DGVPIAYNETHRRLSEETYVVFVETGLSAVYNTIIELAAVKVKDGEII	
DRFMSFANPGHPLSVTTMELTGITDEMVKDAPKPDEVLARFVDWAGDATL	500
VAHNASFDIGFLNAGLARMGRGKIANPVIDTLELARFLYPDLKNHRLNTL	
CCKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFHDELNSRTHSE	600
ASYRLARPFHVTLQAQNETGLKNLFKLVSLSHIQYFHRVPRIPRSVLVKH	
RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIE	700
MDYVKDEEMIKNIIRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIH	
SQGGANPLNRHELDPVYFRTTNEMLDGFSFLGPEKAKEIVDNTQKIASL	800
IGDVKPIKDELYTPRIEGADEEIREMSYRRAKEIYGDPLPKLVEERLEKE	
LKSIIGHGFAVIYLYSHKLVKKSLLDDGYLVGSRGSGVSSFVATMTEITEV	900
NPLPPHYVCPNCKHSEFFNDGSGVSGFDLPDKNCPRCGTKYKKDGHDIFF	
ETFLGFKGDKVPDIDLNFSGEYQPRAHNYTKVLFGEDNVYRAGTIGTVAD	1000
KTAYGEFVKAYASDHNLELRGAEIDLAAGCTGVKRTTGQHPGGIIVVPDYM	
EIYDFTPIQYPADDTSSSEWRTTHFDHFSIHDLNLLKLDILGHDDPTVIRML	1100
QDLSGIDPKTIPTDDPDVMGIFSSTEPLGVTPEQIMCNVGTIGIPEFGTR	
FVRQMLEETRPKTFSELVQISGLSHGTDVWLGNQAELIQNGTCTLSEVIG	1200
CRDDIMVYLIYRGLEPSLAFKIMESVRKGKGLTPEFEAEMRKHDVPEWYI	
DSCKKIKYMFPAKAAAYVLMÄVRIAYFKVHHPLLYYASYFTVRAEDFDL	1300
DAMIKGSPAIRKRIEINAKGIQATAKEKSLTVLEVALEMCEGFSFKN	
IDLYRSQATEFVIDGNSLIPPFNAIPGLGTNVAQAIVRAREEGEFLSKED	1400
LQQRGKLSKTLLEYLESRGCLDSLDPHNQLSLF	

FIG. 89